

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1117	1bor		269	319	1.2e-10	-0.22	0.28		TRANSCRIPTION FACTOR PML; CHAIN: NULL;	TRANSCRIPTION REGULATION PROTO-ONCOGENE, NUCLEAR BODIES (PODS), LEUKEMIA, 2 TRANSCRIPTION REGULATION
1118	1alh	A	366	446	3.6e-33	0.53	0.99		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1118	1alh	A	366	448	3.6e-33			67.71	QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1118	1alh	A	427	526	2.4e-27	0.36	0.65		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1118	1alh	A	474	531	7.2e-20	0.43	0.98		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1118	1mey	C	365	447	2.4e-34			87.59	DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC

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									CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1118	1mey	C	366	446	2.4e-34	0.35	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1118	1mey	C	422	527	1.1e-28	0.29	0.95		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1118	1mey	C	474	531	9.6e-21	0.74	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1118	1mey	G	391	418	1.2e-09	0.68	0.98		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN

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										DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1118	1mey	G	499	526	8.4e-08	0.82	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1118	1tf6	A	365	542	1.2e-41			78.42	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1118	1tf6	A	366	531	1.2e-41	0.22	0.51		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1118	1ubd	C	366	447	3.6e-31	0.27	0.96		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2

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SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1118	1ubd	C	391	526	6e-36	0.15	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1118	1zfd		393	418	0.00036	0.05	0.98		SW15; CHAIN: NULL;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1118	2gli	A	366	528	7.2e-45	0.28	0.77		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER DNA BINDING DOMAIN DNA BINDING MOTIF, ZINC FINGER DNA BINDING DOMAIN
1122	1alh	A	111	191	1.4e-26	0.08	1.00		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1122	1alh	A	22	80	1.7e-17	0.08	-0.18		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN



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SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									SITE; CHAIN: B, C;	FINGER, DNA-BINDING PROTEIN
1122	1alh	A	31	108	1.7e-20	-0.00	-0.09		QGR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1122	1alh	A	363	472	2.4e-42	-0.51	0.48		QGR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1122	1alh	A	84	163	3.4e-23	-0.06	0.19		QGR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1122	1mey	C	110	191	8.5e-45	0.29	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1122	1mey	C	138	219	3.6e-46	0.25	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)

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SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1122	1mey	C	138	219	6.8e-46	0.25	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1122	1mey	C	166	247	1.2e-47	0.39	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1122	1mey	C	166	247	6.8e-47	0.39	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1122	1mey	C	194	275	6e-51	0.50	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1122	1mey	C	194	275	8.5e-48	0.50	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA

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1122	1mey	C	222	303	1.2e-48	0.26	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1122	1mey	C	250	331	8.5e-50	0.20	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1122	1mey	C	278	359	8.5e-51	0.32	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1122	1mey	C	30	108	3.4e-36	0.11	-0.14		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX

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1122	1mey	C	306	387	3.4e-51	0.53	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	(ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1122	1mey	C	306	388	1.7e-51			107.33	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1122	1mey	C	334	415	1.7e-51	0.53	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1122	1mey	C	362	443	1.5e-50	0.13	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1122	1mey	C	390	471	5.1e-50	-0.14	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER	COMPLEX (ZINC FINGER/DNA) ZINC FINGER,

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									PROTEIN; CHAIN: C, F, G;	PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1122	1mey	C	390	499	2.4e-44	-0.32	0.86		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1122	1mey	C	418	499	1.4e-49	0.08	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1122	1mey	C	446	502	8.5e-33	0.21	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1122	1mey	C	57	135	6.8e-38	0.07	-0.07		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL

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1122	1mey	C	83	163	6.8e-41	0.18	0.81		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	STRUCTURE, COMPLEX (ZINC FINGER/DNA)  COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1122	1mey	G	304	331	1.2e-14	0.65	0.99		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1122	1mey	G	304	331	1.7e-13	0.65	0.99		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1122	1mey	G	472	499	1.2e-12	0.06	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1122	1mey	G	472	499	2.4e-13	0.06	1.00		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)

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									CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	FINGER/DNA ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1122	1tf3	A	31	104	1.5e-14	0.10	-0.13		TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)
1122	1tf6	A	111	256	6.8e-35	-0.15	0.77		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1122	1tf6	A	138	304	2.4e-77			109.62	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER

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1122	1ff6	A	139	331	2.4e-77	0.01	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	PROTEIN COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1122	1ff6	A	195	340	3.4e-37	0.18	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1122	1ff6	A	195	359	2.4e-74	-0.07	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1122	1ff6	A	223	415	1.2e-75	-0.17	0.96		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION



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										INITIATION, ZINC FINGER PROTEIN
1122	1tf6	A	307	459	6.8e-38	0.36	0.99		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1122	1tf6	A	307	499	2.4e-72	-0.20	0.72		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1122	1tf6	A	335	481	3.4e-37	-0.17	0.99		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1122	1tf6	A	363	501	8.5e-37	-0.04	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2

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										TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1122	1ubd	C	137	247	4.8e-58	0.18	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1122	1ubd	C	141	247	1.7e-32	0.02	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1122	1ubd	C	174	275	1.7e-32	0.31	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1122	1ubd	C	193	331	2.4e-57	-0.19	0.82		YY1; CHAIN: C; ADENO-	COMPLEX (TRANSCRIPTION REGULATION/DNA)

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SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1122	1ubd	C	202	303	1e-33	-0.09	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1122	1ubd	C	230	331	3.4e-35	0.11	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1122	1ubd	C	258	359	3.4e-36	0.19	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1122	1ubd	C	281	388	9.6e-55			94.96	YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1122	1ubd	C	283	415	9.6e-55	-0.35	0.69		YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1122	1ubd	C	286	387	1.7e-35	0.16	1.00		YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1122	1ubd	C	33	135	3.4e-24	0.22	-0.15		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1122	1ubd	C	342	443	3.4e-35	0.25	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1122	1ubd	C	360	499	2.4e-54	-0.35	0.63		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1122	1ubd	C	398	499	1.7e-34	-0.22	0.93		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1122	1ubd	C	60	163	8.5e-27	-0.18	0.07		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1122	1ubd	C	86	191	3.4e-31	0.07	0.64		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1122	2gli	A	130	276	3.6e-60	-0.02	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1122	2gli	A	138	333	1.2e-75	-0.20	0.81		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1122	2gli	A	202	330	1.2e-33	0.06	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1122	2gli	A	250	389	7.2e-70			99.38	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1122	2gli	A	306	473	7.2e-70	-0.05	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1122	2gli	A	314	442	3.4e-34	0.57	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1122	2gli	A	342	470	5.1e-34	0.31	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1122	2gli	A	370	498	1.5e-33	0.17	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1122	2gli	A	83	218	3.4e-31	0.31	0.83		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	BINDING PROTEIN/DNA) COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE- FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)
1124	1a8h		37	523	1.7e-46			70.99	METHIONYL-TRNA SYNTHETASE; CHAIN: NULL;	AMINOACYL-TRNA SYNTHETASE METRS; AMINOACYL-TRNA SYNTHETASE, ROSSMANN FOLD
1124	1gln		36	522	1e-76			340.16	GLUTAMYL-TRNA SYNTHETASE; 1GLN 4 CHAIN: NULL 1GLN 5	AMINOACYL-TRNA SYNTHASE
1124	1gln		37	522	1e-76	0.53	1.00		GLUTAMYL-TRNA SYNTHETASE; 1GLN 4 CHAIN: NULL 1GLN 5	AMINOACYL-TRNA SYNTHASE
1124	1qtq	A	18	523	6.8e-52			109.90	GLUTAMINYL-TRNA SYNTHETASE; CHAIN: A; TRNA GLN II; CHAIN: B;	COMPLEX (TRNA SYNTHETASE/TRNA) GLNRS; TRNA SYNTHETASE, GLUTAMINE, TRNAGLN, E. COLI, COMPLEX
1124	1qtq	A	23	495	6.8e-52	-0.05	0.40		GLUTAMINYL-TRNA SYNTHETASE; CHAIN: A; TRNA GLN II; CHAIN: B;	COMPLEX (TRNA SYNTHETASE/TRNA) GLNRS; TRNA SYNTHETASE, GLUTAMINE, TRNAGLN, E. COLI, COMPLEX



Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1128	1pdn	C	75	195	5.1e-34	0.45	1.00		PRD PAIRED DOMAIN; CHAIN: C; 1PDN 4 DNA; CHAIN: A, B 1PDN 5	COMPLEX (GENE REGULATING PROTEIN/DNA) PAX, PRD, PAIRED DOMAIN, DNA-BINDING PROTEIN 1PDN 14
1128	1pdn	C	75	197	6.6e-65			169.42	PRD PAIRED DOMAIN; CHAIN: C; 1PDN 4 DNA; CHAIN: A, B 1PDN 5	COMPLEX (GENE REGULATING PROTEIN/DNA) PAX, PRD, PAIRED DOMAIN, DNA-BINDING PROTEIN 1PDN 14
1128	1pdn	C	76	197	6.6e-65	0.68	1.00		PRD PAIRED DOMAIN; CHAIN: C; 1PDN 4 DNA; CHAIN: A, B 1PDN 5	COMPLEX (GENE REGULATING PROTEIN/DNA) PAX, PRD, PAIRED DOMAIN, DNA-BINDING PROTEIN 1PDN 14
1128	6pax	A	74	206	1.1e-70			165.42	HOMEBOX PROTEIN PAX-6; CHAIN: A; 26 NUCLEOTIDE DNA; CHAIN: B; 26 NUCLEOTIDE DNA; CHAIN: C;	GENE REGULATION/DNA PAX, PAIRED DOMAIN, TRANSCRIPTION, PROTEIN-DNA INTERACTIONS, 2 GENE REGULATION/DNA
1128	6pax	A	74	206	1.1e-70	0.50	1.00		HOMEBOX PROTEIN PAX-6; CHAIN: A; 26 NUCLEOTIDE DNA; CHAIN: B; 26 NUCLEOTIDE DNA; CHAIN: C;	GENE REGULATION/DNA PAX, PAIRED DOMAIN, TRANSCRIPTION, PROTEIN-DNA INTERACTIONS, 2 GENE REGULATION/DNA
1128	6pax	A	75	206	5.1e-39	0.42	1.00		HOMEBOX PROTEIN PAX-6; CHAIN: A; 26 NUCLEOTIDE DNA; CHAIN: B; 26 NUCLEOTIDE DNA; CHAIN: C;	GENE REGULATION/DNA PAX, PAIRED DOMAIN, TRANSCRIPTION, PROTEIN-DNA INTERACTIONS, 2 GENE REGULATION/DNA

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1132	1a17		1270	1378	0.00084	-0.41	0.04		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRATRICPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN- PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE
1132	1aww		4	64	2.4e-07	0.05	0.76		BRUTON'S TYROSINE KINASE; CHAIN: NULL;	TRANSFERASE ATK, AMGX1, BPK; TYROSINE KINASE, X-LINKED AGAMMAGLOBULINEMIA, XLA, BTK, SH3 2 DOMAIN, TRANSFERASE
1132	1bbz	A	14	68	9.6e-08	0.29	0.34		ABL TYROSINE KINASE; CHAIN: A, C, E, G; PEPTIDE P41; CHAIN: B, D, F, H;	COMPLEX (TRANSFERASE/PEPTIDE) COMPLEX (TRANSFERASE/PEPTIDE), SIGNAL TRANSDUCTION, 2 SH3 DOMAIN
1132	1cka	A	14	64	7.2e-08	0.05	0.34		COMPLEX (ONCOGENE PROTEIN/PEPTIDE) C-CRK (N- TERMINAL SH3 DOMAIN) (C- CRK SH3-N) COMPLEXED WITH 1CKA 3 C3G PEPTIDE (PRO-PRO- PRO-ALA-LEU-PRO-PRO-LYS- LYS-ARG) 1CKA 4	
1132	1csk	A	11	67	7.2e-08	1.01	0.62		PHOSPHOTRANSFERASE C-SRC KINASE (SH3 DOMAIN) (E.C.2.7.1.112) 1CSK 3	
1132	1fyn	A	14	68	1.2e-07	0.21	0.22		PHOSPHOTRANSFERASE FYN; CHAIN: A; 3BP-2; CHAIN: B;	TRANSFERASE PROTO- ONCOGENE TYROSINE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										KINASE; PROTO-ONCOGENE, TRANSFERASE, TYROSINE-PROTEIN KINASE, 2 PHOSPHORYLATION, ATP-BINDING, MYRISTYLATION, SH3 DOMAIN, 3 COMPLEX (PHOSPHOTRANSFERASE/PEPTIDE)
1132	1shf	A	14	68	2.4e-07	0.33	0.66		PHOSPHOTRANSFERASE FYN PROTO-ONCOGENE TYROSINE KINASE (E.C.2.7.1.112) 1SHF 3 (SH3 DOMAIN) 1SHF 4	
1132	4hck		10	68	1.2e-08	0.12	0.22		HEMATOPOIETIC CELL KINASE; CHAIN: NULL;	TRANSFERASE HCK; SH3, PROTEIN TYROSINE KINASE, SIGNAL TRANSDUCTION, 2 TRANSFERASE
1137	1cfe		7	119	1.7e-38			52.74	PATHOGENESIS-RELATED PROTEIN P14A; CHAIN: NULL;	PATHOGENESIS-RELATED PROTEIN PATHOGENESIS-RELATED LEAF PROTEIN 6, ETHYLENE PATHOGENESIS-RELATED PROTEIN, PR-1 PROTEINS, 2 PLANT DEFENSE
1137	1cfe		7	119	1.7e-38	0.52	1.00		PATHOGENESIS-RELATED PROTEIN P14A; CHAIN: NULL;	PATHOGENESIS-RELATED PROTEIN PATHOGENESIS-RELATED LEAF PROTEIN 6, ETHYLENE PATHOGENESIS-RELATED PROTEIN, PR-1

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1137	1qnx	A	1	122	1.7e-29	0.44	0.99		VES V 5; CHAIN: A;	PROTEINS, 2 PLANT DEFENSE ALLERGEN ANTIGEN 5; ANTIGEN 5, ALLERGEN, VESPID VENOM
1138	1a4y	A	124	286	1.7e-10	-0.21	0.05		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS
1138	1a4y	A	183	303	6e-07	0.54	0.69		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS
1138	1a4y	A	212	308	6.8e-06	0.07	0.00		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1138	1d0b	A	165	308	6.8e-19	-0.34	0.04		INTERVALIN B; CHAIN: A;	MAPPING, LEUCINE-RICH 3 REPEATS
1138	1dce	A	198	308	1e-08	-0.27	0.01		RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B, D;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1141	1a12	A	1	376	1.4e-63			90.00	REGULATOR OF CHROMOSOME CONDENSATION 1; CHAIN: A, B, C;	GUANINE NUCLEOTIDE EXCHANGE FACTOR RCC1; GUANINE NUCLEOTIDE EXCHANGE FACTOR, GEF, RAN, 2 RAS-LIKE NUCLEAR GTP BINDING PROTEIN HEADER TER
1141	1a12	A	20	376	1.4e-63	0.50	0.93		REGULATOR OF CHROMOSOME CONDENSATION 1; CHAIN: A, B, C;	GUANINE NUCLEOTIDE EXCHANGE FACTOR RCC1; GUANINE NUCLEOTIDE EXCHANGE FACTOR, GEF, RAN, 2 RAS-LIKE NUCLEAR GTP BINDING PROTEIN HEADER TER
1145	1pfx	L	236	280	0.0006	-0.15	0.06		FACTOR IXA; CHAIN: C, L; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
1148	1a5e		581	696	3.4e-21	0.81	0.94		TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT
1148	lawc	B	425	555	6.8e-28	0.09	0.12		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING; 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1148	lawc	B	482	629	4.8e-30	0.40	0.98		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING; 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1148	lawc	B	508	663	3.4e-38	0.32	0.95		GA BINDING PROTEIN ALPHA;	COMPLEX (TRANSCRIPTION

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1148	1awc	B	542	696	8.5e-38	0.74	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1148	1bd8		451	599	8.5e-26	0.26	0.98		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1148	1bd8		504	667	1.2e-36	0.66	1.00		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1148	1bd8		511	666	3.4e-33	0.56	1.00		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1148	1bd8		545	699	1e-27	0.43	0.99		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										CDK4/6 INHIBITOR, ANKYRIN MOTIF
1148	1bi7	B	504	630	3.6e-25	0.73	0.96		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; MULTIPLE TUMOR SUPPRESSOR; CHAIN: B;	COMPLEX (KINASE/ANTI-ONCOGENE) CDK6; P16INK4A, MTS1; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, MULTIPLE TUMOR SUPPRESSOR, 3 MTS1, COMPLEX (KINASE/ANTI-ONCOGENE) HEADER
1148	1bi7	B	581	696	5.1e-22	0.70	0.98		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; MULTIPLE TUMOR SUPPRESSOR; CHAIN: B;	COMPLEX (KINASE/ANTI-ONCOGENE) CDK6; P16INK4A, MTS1; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, MULTIPLE TUMOR SUPPRESSOR, 3 MTS1, COMPLEX (KINASE/ANTI-ONCOGENE) HEADER
1148	1blx	B	545	699	6.8e-27	0.33	0.99		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR



Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1148	1bu9	A	425	568	5.1e-25	0.19	0.23		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	PROTEIN(KINASE) HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1148	1bu9	A	474	628	3.4e-28	0.67	0.95		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1148	1bu9	A	508	668	1.7e-36	0.47	0.25		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1148	1bu9	A	555	701	3.4e-34	0.83	0.58		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1148	1cun	A	68	285	3.6e-05	0.15	0.36		ALPHA SPECTRIN; CHAIN: A, B, C;	HORMONE/GROWTH FACTOR STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1148	1d9s	A	497	636	2.4e-32	0.49	0.82		CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT
1148	1d9s	A	581	696	5.1e-22	0.90	0.60		CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT
1148	1dcq	A	612	699	6.8e-17	0.56	0.62		PYK2-ASSOCIATED PROTEIN BETA; CHAIN: A;	METAL BINDING PROTEIN ZINC-BINDING MODULE, ANKYRIN REPEATS, METAL BINDING PROTEIN
1148	1hhb	A	474	628	3.4e-28	0.56	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18- INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1148	1hhb	A	508	667	8.5e-36	0.56	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18- INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ. FOLD score	Compound	PDB annotation
1148	1hhb	A	555	700	1.7e-33	0.82	0.96		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1148	1ikn	D	434	580	5.1e-29	-0.09	0.00		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1148	1ikn	D	503	696	1.7e-39	0.65	1.00		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1148	1myo		582	696	3.4e-24	0.43	0.69		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT
1148	1myo		615	701	1.2e-17	0.20	0.15		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT
1148	1nfi	E	427	580	1.7e-29	-0.03	0.00		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1148	1nfi	E	502	696	3.4e-39	0.67	1.00		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1148	1ycs	B	581	696	6.8e-19	0.67	1.00		P53; CHAIN: A; 53BP2; CHAIN: B;	COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS) P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS)
1148	1ycs	B	636	701	1.7e-19	0.36	0.09		P53; CHAIN: A; 53BP2; CHAIN: B;	COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS) P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS)
1153	1a7j		162	221	2.4e-12	0.35	0.63		OCRP2 (LIM1); CHAIN: NULL;	LIM DOMAIN CONTAINING

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1153	1b8t	A	155	217	6e-12	0.54	0.71		CRP1; CHAIN: A;	PROTEINS LIM DOMAIN CONTAINING PROTEINS, METAL-BINDING PROTEIN, ZINC 2 FINGER
1153	1bhd	A	5	105	1.4e-36	0.76	1.00		UTROPHIN; CHAIN: A, B;	CONTRACTILE LIM DOMAIN, CRP, NMR, MUSCLE DIFFERENTIATION, CONTRACTILE
1153	1bkr	A	2	110	6.8e-47			104.59	SPECTRIN BETA CHAIN; CHAIN: A;	STRUCTURAL PROTEIN CALPONIN HOMOLOGY, ACTIN BINDING, STRUCTURAL PROTEIN
1153	1bkr	A	4	110	6.8e-47	0.82	1.00		SPECTRIN BETA CHAIN; CHAIN: A;	ACTIN-BINDING CALPONIN HOMOLOGY (CH) DOMAIN; FILAMENTOUS ACTIN-BINDING DOMAIN, CYTOSKELETON
1153	1ctl		161	217	1.2e-10	0.69	0.96		AVIAN CYSTEINE RICH PROTEIN; 1CTL 3	METAL-BINDING PROTEIN LIM DOMAIN CONTAINING PROTEINS 1CTL 15
1153	1cxx	A	161	220	2.4e-11	0.58	0.69		CYSTEINE AND GLYCINE-RICH PROTEIN CRP2; CHAIN: A;	SIGNALING PROTEIN LIM DOMAIN CONTAINING PROTEINS, METAL-BINDING PROTEIN
1153	1dxx	A	5	110	5.1e-37	0.84	1.00		DYSTROPHIN; CHAIN: A, B, C, D;	STRUCTURAL PROTEIN DYSTROPHIN, MUSCULAR

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1153	1qag	A	5	109	3.4e-37	0.64	1.00		UTROPHIN ACTIN BINDING REGION; CHAIN: A, B;	DYSTROPHY, CALPONIN HOMOLOGY DOMAIN, 2 ACTIN-BINDING, UTROPHIN STRUCTURAL PROTEIN CALPONIN HOMOLOGY DOMAIN, DOMAIN SWAPPING, ACTIN BINDING, 2 UTROPHIN, DYSTROPHIN, STRUCTURAL PROTEIN
1153	1zfo		161	189	4.8e-05	-0.45	0.49		LASP-1; CHAIN: NULL;	METAL-BINDING PROTEIN LIM DOMAIN, ZINC-FINGER, METAL-BINDING PROTEIN
1155	1e19	A	11	207	1.7e-33	-0.37	0.09		CARBAMATE KINASE-LIKE CARBAMOYLPHOSPHATE SYNTHETASE; CHAIN: A;	TRANSFERASE PYROCOCUS FURIOSUS, HYPERTHERMOPHILES, ADP SITE, 2 PHOSPHORYL GROUP TRANSFER, ARGININE METABOLISM
1156	1aj4		102	273	1.7e-44			57.30	TROPONIN C; CHAIN: NULL;	MUSCLE PROTEIN CTNC; CARDIAC, MUSCLE PROTEIN, REGULATORY, CALCIUM BINDING
1156	1aj4		110	270	1.7e-44	-0.00	0.59		TROPONIN C; CHAIN: NULL;	MUSCLE PROTEIN CTNC; CARDIAC, MUSCLE PROTEIN, REGULATORY, CALCIUM BINDING
1156	1aj4		198	350	1.7e-42	0.25	0.54		TROPONIN C; CHAIN: NULL;	MUSCLE PROTEIN CTNC; CARDIAC, MUSCLE PROTEIN, REGULATORY,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1156	1aui	B	203	355	1.5e-34	0.06	0.70		SERINE/THREONINE PHOSPHATASE 2B; CHAIN: A, B;	CALCIUM BINDING
1156	1cdm	A	112	270	3.4e-53	-0.05	0.99		CALCIUM-BINDING PROTEIN CALMODULIN COMPLEXED WITH CALMODULIN-BINDING DOMAIN OF 1CDM 3 CALMODULIN-DEPENDENT PROTEIN KINASE II 1CDM 4	HYDROLASE CALCINEURIN; HYDROLASE, PHOSPHATASE, IMMUNOSUPPRESSION
1156	1cdm	A	201	346	8.5e-52	0.14	0.99		CALCIUM-BINDING PROTEIN CALMODULIN COMPLEXED WITH CALMODULIN-BINDING DOMAIN OF 1CDM 3 CALMODULIN-DEPENDENT PROTEIN KINASE II 1CDM 4	
1156	1cdm	A	280	371	1.2e-28	-0.17	0.00		CALCIUM-BINDING PROTEIN CALMODULIN COMPLEXED WITH CALMODULIN-BINDING DOMAIN OF 1CDM 3 CALMODULIN-DEPENDENT PROTEIN KINASE II 1CDM 4	
1156	1cll		112	270	5.1e-58	0.31	0.99		CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE) 1CLL 3	
1156	1cll		196	348	6.8e-56			56.73	CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE) 1CLL 3	
1156	1cll		201	346	6.8e-56	-0.10	0.84		CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE)	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1156	1cll		280	371	6.8e-29	0.03	0.11		1CLL 3 CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE)	
1156	1cmf		278	346	3.4e-30	0.11	0.72		1CLL 3 CALMODULIN (VERTEBRATE); 1CMF 6 CHAIN: NULL; 1CMF 7	CALCIUM-BINDING PROTEIN CALMODULIN APO TR2C-DOMAIN; 1CMF 9
1156	1dtl	A	110	270	8.5e-42	0.14	1.00		CARDIAC TROPONIN C; CHAIN: A;	STRUCTURAL PROTEIN HELIX-TURN-HELIX
1156	1dtl	A	198	349	3.4e-38	-0.07	0.98		CARDIAC TROPONIN C; CHAIN: A;	STRUCTURAL PROTEIN HELIX-TURN-HELIX
1156	1exr	A	110	271	3.4e-56	0.31	0.96		CALMODULIN; CHAIN: A;	METAL TRANSPORT CALMODULIN, HIGH RESOLUTION, DISORDER
1156	1exr	A	198	346	1.7e-54	0.16	0.86		CALMODULIN; CHAIN: A;	METAL TRANSPORT CALMODULIN, HIGH RESOLUTION, DISORDER
1156	1f71	A	283	346	1.4e-29	0.31	1.00		CALMODULIN; CHAIN: A;	TRANSPORT PROTEIN CALCIUM BINDING, EF HAND, FOUR-HELIX BUNDLE
1156	1tcf		109	269	3.4e-48	0.26	0.94		TROPONIN C; CHAIN: NULL;	CALCIUM-REGULATED MUSCLE CONTRACTION MUSCLE CONTRACTION, CALCIUM-BINDING, TROPONIN, E-F HAND, 2 OPEN CONFORMATION REGULATORY DOMAIN, CALCIUM-REGULATED 3 MUSCLE CONTRACTION
1156	1tcf		194	347	3.4e-45			59.86	TROPONIN C; CHAIN: NULL;	CALCIUM-REGULATED MUSCLE CONTRACTION



Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										MUSCLE CONTRACTION MUSCLE CONTRACTION, CALCIUM-BINDING, TROPONIN, E-F HAND, 2 OPEN CONFORMATION REGULATORY DOMAIN, CALCIUM-REGULATED 3 MUSCLE CONTRACTION
1156	1trf		201	346	3.4e-45	-0.01	0.86		TROPONIN C; CHAIN: NULL;	CALCIUM-REGULATED MUSCLE CONTRACTION MUSCLE CONTRACTION, CALCIUM-BINDING, TROPONIN, E-F HAND, 2 OPEN CONFORMATION REGULATORY DOMAIN, CALCIUM-REGULATED 3 MUSCLE CONTRACTION
1156	1tnx		111	269	8.5e-46	-0.15	0.70		TROPONIN C; 1TNX 4 CHAIN: NULL; 1TNX 5	CALCIUM-BINDING PROTEIN EF-HAND 1TNX 14
1156	1tnx		194	346	1.5e-41			55.58	TROPONIN C; 1TNX 4 CHAIN: NULL; 1TNX 5	CALCIUM-BINDING PROTEIN EF-HAND 1TNX 14
1156	1tnx		199	346	1.5e-41	0.15	1.00		TROPONIN C; 1TNX 4 CHAIN: NULL; 1TNX 5	CALCIUM-BINDING PROTEIN EF-HAND 1TNX 14
1156	1tnx		279	371	3.4e-26	0.00	0.03		TROPONIN C; 1TNX 4 CHAIN: NULL; 1TNX 5	CALCIUM-BINDING PROTEIN EF-HAND 1TNX 14
1156	1top		111	269	5.1e-49	0.19	1.00		CONTRACTILE SYSTEM PROTEIN TROPONIN C 1TOP 3	
1156	1top		199	350	6.8e-46	0.26	0.77		CONTRACTILE SYSTEM PROTEIN TROPONIN C 1TOP 3	
1156	1top		99	273	5.1e-49			57.55	CONTRACTILE SYSTEM PROTEIN TROPONIN C 1TOP 3	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1156	1trc	A	281	346	1e-29	-0.24	0.68		CALCIUM BINDING PROTEIN CALMODULIN (TR=2=C\$ FRAGMENT COMPRISING RESIDUES 78 - 148 1TRC 3 OF THE INTACT MOLECULE) 1TRC 4	
1156	1vrk	A	109	272	8.5e-57	0.01	0.94		CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)
1156	1vrk	A	193	344	8.5e-57			56.98	CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)
1156	1vrk	A	198	347	3.4e-55	0.20	0.99		CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)
1156	1vrk	A	27	183	8.5e-45	0.03	-0.17		CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)
1156	1vrk	A	285	371	3.4e-28	0.13	0.17		CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1156	2sas		89	288	8e-20			50.84	CALCIUM-BINDING PROTEIN SARCOPHILIN CALCIUM-BINDING PROTEIN (ISO TYPE II) 2SAS 3	
1157	1cum	A	80	286	4.8e-10	-0.15	0.07		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1157	1f5n	A	222	355	0.0072	-0.58	0.05		INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1; CHAIN: A;	SIGNALING PROTEIN GBP, GTP HYDROLYSIS, GDP, GMP, INTERFERON INDUCED, DYNAMIN 2 RELATED, LARGE GTPASE FAMILY. GMPNP, GPPNHP.
1157	1fqv	A	132	308	0.0096	-0.25	0.04		SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P;	LIGASE CYCLIN A/CDK2-ASSOCIATED PROTEIN P45; CYCLIN A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
1157	1qqe	A	19	244	7.2e-14	-0.17	0.00		VESICULAR TRANSPORT PROTEIN SEC17; CHAIN: A;	PROTEIN TRANSPORT HELIX-TURN-HELIX TPR-LIKE REPEAT, PROTEIN TRANSPORT

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
11157	1quu	A	97	355	3.6e-23	-0.16	0.13		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
11159	1d5r	A	28	256	3.4e-20	-0.10	0.33		PHOSPHOINOSITIDE PHOSPHOTASE PTEN; CHAIN: A;	HYDROLASE C2 DOMAIN, PHOSPHOTIDYLINOSITOL, PHOSPHOTASE, HYDROLASE
11159	1mkp		59	206	1.4e-16	0.06	0.45		PYST1; CHAIN: NULL;	HYDROLASE DUAL SPECIFICITY PHOSPHATASE, MAP KINASE HYDROLASE
11159	2slp	A	3	207	3.4e-57	-0.16	0.01		SHP-2; CHAIN: A, B;	TYROSINE PHOSPHATASE SYP, SHPTP-2; TYROSINE PHOSPHATASE, INSULIN SIGNALING, SH2 PROTEIN
11165	1a25	A	222	348	1.7e-28	0.76	0.57		PROTEIN KINASE C (BETA); CHAIN: A, B;	CALCIUM-BINDING PROTEIN CALB; CALCIUM++/PHOSPHOLIPID BINDING PROTEIN, 2 CALCIUM-BINDING PROTEIN
11165	1a25	A	367	470	7.2e-11	0.15	0.04		PROTEIN KINASE C (BETA); CHAIN: A, B;	CALCIUM-BINDING PROTEIN CALB; CALCIUM++/PHOSPHOLIPID BINDING PROTEIN, 2 CALCIUM-BINDING PROTEIN
11165	1a25	A	389	476	5.1e-26	0.13	-0.05		PROTEIN KINASE C (BETA);	CALCIUM-BINDING

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									CHAIN: A, B;	PROTEIN CALB; CALCIUM++/PHOSPHOLIPID BINDING PROTEIN, 2 CALCIUM-BINDING PROTEIN
1165	1byn	A	222	348	3.4e-35	0.64	0.75		SYNAPTOTAGMIN I; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN, C2- DOMAIN, EXOCYTOSIS, NEUROTRANSMITTER 2 RELEASE, ENDOCYTOSIS/EXOCYTOSIS
1165	1byn	A	389	473	6.8e-16	-0.04	0.16		SYNAPTOTAGMIN I; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN, C2- DOMAIN, EXOCYTOSIS, NEUROTRANSMITTER 2 RELEASE, ENDOCYTOSIS/EXOCYTOSIS
1165	1cyj	A	237	335	5.1e-16	0.35	-0.01		CYTOSOLIC PHOSPHOLIPASE A2; CHAIN: A, B;	HYDROLASE CPLA2; PHOSPHOLIPASE, LIPID- BINDING, HYDROLASE
1165	1cyj	A	389	466	1.4e-09	-0.35	0.19		CYTOSOLIC PHOSPHOLIPASE A2; CHAIN: A, B;	HYDROLASE CPLA2; PHOSPHOLIPASE, LIPID- BINDING, HYDROLASE
1165	1dix	A	239	359	3.4e-24	0.50	-0.09		PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B;	LIPID DEGRADATION PLC- D1; PHOSPHORIC DIESTER HYDROLASE, HYDROLASE, LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM- BINDING, PHOSPHOLIPASE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										C, 3 PHOSPHOINOSITIDE-SPECIFIC
1165	1dix	A	389	479	6.8e-19	0.16	0.04		PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B;	LIPID DEGRADATION PLC-D1; PHOSPHORIC DIESTER HYDROLASE, HYDROLASE, 2 LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3 PHOSPHOINOSITIDE-SPECIFIC
1165	1dix	B	239	359	3.4e-24	0.69	-0.08		PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B;	LIPID DEGRADATION PLC-D1; PHOSPHORIC DIESTER HYDROLASE, HYDROLASE, 2 LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3 PHOSPHOINOSITIDE-SPECIFIC
1165	1dix	B	389	479	6.8e-19	-0.13	0.00		PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B;	LIPID DEGRADATION PLC-D1; PHOSPHORIC DIESTER HYDROLASE, HYDROLASE, 2 LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3 PHOSPHOINOSITIDE-SPECIFIC
1165	1dqv	A	122	358	6.8e-50	0.16	0.05		SYNAPTOTAGMIN III; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS BETA SANDWICH, CALCIUM ION, C2 DOMAIN
1165	1dqv	A	224	487	5.1e-63	0.19	0.98		SYNAPTOTAGMIN III; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS BETA SANDWICH,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1165	1dsy	A	221	351	6.8e-31	0.45	0.13		PROTEIN KINASE C, ALPHA TYPE; CHAIN: A;	CALCIUM ION, C2 DOMAIN TRANSFERASE CALCIUM++, PHOSPHOLIPID BINDING PROTEIN, CALCIUM-BINDING 2 PROTEIN, PHOSPHATIDYL SERINE, PROTEIN KINASE C
1165	1dsy	A	367	470	3.6e-11	0.19	0.03		PROTEIN KINASE C, ALPHA TYPE; CHAIN: A;	TRANSFERASE CALCIUM++, PHOSPHOLIPID BINDING PROTEIN, CALCIUM-BINDING 2 PROTEIN, PHOSPHATIDYL SERINE, PROTEIN KINASE C
1165	1dsy	A	389	476	3.4e-26	-0.09	0.01		PROTEIN KINASE C, ALPHA TYPE; CHAIN: A;	TRANSFERASE CALCIUM++, PHOSPHOLIPID BINDING PROTEIN, CALCIUM-BINDING 2 PROTEIN, PHOSPHATIDYL SERINE, PROTEIN KINASE C
1165	1rlw		237	335	5.1e-16	0.11	-0.01		PHOSPHOLIPASE A2; CHAIN: NULL;	HYDROLASE CALB DOMAIN; HYDROLASE, C2 DOMAIN, CALB DOMAIN
1165	1rsy		222	340	6.8e-35	0.57	0.74		CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) IRSY 3	
1165	1rsy		389	473	6.8e-16	0.17	0.01		CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) IRSY 3	
1165	3rpb	A	224	355	8.5e-25	0.47	0.04		RABPHILIN 3-A; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										S C2-DOMAINS, C2B-DOMAIN, RABPHILIN, ENDOCYTOSIS/EXOCYTOSIS
1165	3pb	A	357	488	6.8e-29	0.40	0.13		RABPHILIN 3-A; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS C2-DOMAINS, C2B-DOMAIN, RABPHILIN, ENDOCYTOSIS/EXOCYTOSIS
1172	1alh	A	135	208	3.4e-26	0.26	1.00		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1172	1alh	A	135	209	2e-26	0.28	0.98		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1172	1alh	A	296	376	1.7e-30	0.50	1.00		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1172	1alh	A	296	378	6e-44			76.10	QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1172	1alh	A	296	378	6e-44	0.27	1.00		QGSZ ZINC FINGER PEPTIDE;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN



Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1172	1mey	C	102	180	3.4e-37	0.27	0.03		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1172	1mey	C	128	208	1.7e-44	0.22	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1172	1mey	C	155	236	1.5e-48	0.80	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1172	1mey	C	183	264	6.8e-50	0.59	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1172	1mey	C	183	265	3.4e-50			102.15	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	(ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1172	1mey	C	211	292	3.4e-50	0.75	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1172	1mey	C	239	320	3.4e-50	0.54	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1172	1mey	C	267	348	8.5e-51	0.73	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1172	1mey	C	295	376	1.2e-50	0.57	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER	COMPLEX (ZINC FINGER/DNA) ZINC FINGER,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									PROTEIN; CHAIN: C, F, G;	PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1172	1mey	C	323	405	8.5e-49	0.08	0.76		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1172	1tf6	A	109	245	5.1e-30	0.07	0.46		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1172	1tf6	A	131	292	2e-57	-0.03	0.98		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1172	1tf6	A	135	273	8.5e-34	0.52	0.63		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1172	1ff6	A	183	349	1.4e-72			104.46	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1172	1ff6	A	184	329	5.1e-37	0.26	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1172	1ff6	A	212	376	1.4e-72	0.27	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1172	1ff6	A	268	418	8e-44	-0.13	0.90		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1172	1ff6	A	296	454	6.8e-37	-0.24	0.57		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1172	1ubd	C	110	208	3.4e-29	0.21	0.71		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1172	1ubd	C	128	236	4e-39	0.19	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1172	1ubd	C	135	236	8.5e-33	0.47	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	REGULATION/DNA COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1172	1ubd	C	163	264	1.4e-34	0.50	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1172	1ubd	C	182	292	1.6e-52	0.43	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1172	1ubd	C	219	320	5.1e-34	0.18	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									CHAIN: A, B;	INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1172	1ubd	C	241	349	6e-54			84.85	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1172	1ubd	C	265	376	6e-54	0.02	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1172	1ubd	C	293	390	1.8e-38	0.04	0.88		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1172	1ubd	C	303	406	1.7e-32	-0.00	0.16		YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA)
1172	1ubd	C	331	438	1.5e-29	-0.43	0.10		YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1172	1ubd	C	90	180	1e-21	0.08	-0.15		YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1172	2gli	A	107	235	1.7e-32	0.39	0.78		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-



Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1172	2gli	A	128	263	3.4e-34	0.60	0.98		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1172	2gli	A	135	266	8e-52	0.27	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1172	2gli	A	157	294	2e-69			93.54	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1172	2gli	A	183	350	2e-67	0.49	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1172	2gli	A	211	376	2e-69	0.05	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1172	2gli	A	275	406	1e-32	-0.08	0.36		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1174	1alh	A	1	70	1.4e-27			52.45	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLICATION OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1174	1alh	A	16	86	6.8e-26	0.37	0.94		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLICATION OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1174	1alh	A	4	70	1.7e-25	0.50	1.00		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLICATION OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1174	1alh	A	5	70	1.4e-27	0.57	1.00		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLICATION OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1174	1mey	C	15	125	6.8e-44	0.11	0.05		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1174	1mey	C	15	96	6.8e-44			63.59	DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1174	1mey	C	3	68	6.8e-39	0.39	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1174	1mey	G	182	209	5.1e-13	0.08	-0.05		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1174	1ubd	C	164	246	5.1e-27	0.05	-0.19		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1174	1ubd	C	3	125	1.7e-27	-0.08	0.21		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									INITIATOR ELEMENT DNA; CHAIN: A, B;	YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1174	2adr		16	76	1.5e-17			54.11	ADR1; CHAIN: NULL;	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION REGULATION, ADR1, ZINC FINGER, NMR
1174	2gli	A	5	127	6.8e-27	-0.13	0.16		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1176	1alh	A	107	158	0.00018	-0.53	0.09		QGR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1176	1mey	C	107	158	0.0014	-0.65	0.07		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1176	1tf6	A	107	158	0.00014	-0.57	0.24		TFIIIA; CHAIN: A, D; 5S	COMPLEX (TRANSCRIPTION

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1176	2adr		107	159	0.0004	-0.31	0.03		ADR1; CHAIN: NULL;	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ADR1, ZINC FINGER, NMR
1180	1csk	A	518	572	4.8e-13	0.28	0.76		PHOSPHOTRANSFERASE C-SRC KINASE (SH3 DOMAIN) (E.C.2.7.1.112) 1CSK 3	
1180	1f5x	A	172	340	2.4e-33	0.11	0.80		RHO-GEF VAV; CHAIN: A;	SIGNALING PROTEIN 11 ALPHA-HELICES
1180	1fmk		517	596	6.8e-19	0.16	0.12		TYROSINE-PROTEIN KINASE SRC; CHAIN: NULL;	PHOSPHOTRANSFERASE C-SRC, P60-SRC; SRC, TYROSINE KINASE, PHOSPHORYLATION, SH2, SH3, 2 PHOSPHOTYROSINE, PROTO-ONCOGENE, PHOSPHOTRANSFERASE
1180	1fyn	A	513	573	2.4e-14	0.50	0.59		PHOSPHOTRANSFERASE FYN; CHAIN: A; 3BP-2; CHAIN: B;	TRANSFERASE PROTO-ONCOGENE TYROSINE KINASE; PROTO-ONCOGENE, TRANSFERASE, TYROSINE-PROTEIN KINASE, 2

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										PHOSPHORYLATION, ATP-BINDING, MYRISTYLATION, SH3 DOMAIN, 3 COMPLEX (PHOSPHOTRANSFERASE/PEPTIDE)
1180	1fyn	A	514	574	1.4e-12	0.18	0.78		PHOSPHOTRANSFERASE FYN; CHAIN: A; 3BP-2; CHAIN: B;	TRANSFERASE PROTO-ONCOGENE TYROSINE KINASE; PROTO-ONCOGENE, TRANSFERASE, TYROSINE-PROTEIN KINASE, 2
										PHOSPHORYLATION, ATP-BINDING, MYRISTYLATION, SH3 DOMAIN, 3 COMPLEX (PHOSPHOTRANSFERASE/PEPTIDE)
1180	1gfc		517	573	1.2e-12	0.29	0.69		ADAPTOR PROTEIN CONTAINING SH2 AND SH3 GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2 (GRB2) 1GFC 3 (C-TERMINAL SH3 DOMAIN) (NMR, MINIMIZED MEAN STRUCTURE) 1GFC 4	
1180	1lck	A	524	598	3.4e-13	-0.00	0.01		P56=LCK= TYROSINE KINASE; 1LCK 7 CHAIN: A; 1LCK 8 TAIL PHOSHOPEPTIDE TEGQ(PHOSHO)YQPQPA; 1LCK 14 CHAIN: B; 1LCK 15	COMPLEX (KINASE/PEPTIDE)
1180	1pwt		513	573	1.2e-12	0.35	0.87		ALPHA SPECTRIN; CHAIN: NULL;	CIRCULAR PERMUTANT PWT; CIRCULAR PERMUTANT, SH3 DOMAIN,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1180	1qcf	A	513	598	3.4e-16	-0.18	0.07		HAEMATOPOIETIC CELL KINASE (HCK); CHAIN: A;	CYTOSKELETON TYROSINE KINASE TYROSINE KINASE-INHIBITOR COMPLEX, DOWN-REGULATED KINASE, 2 ORDERED ACTIVATION LOOP
1180	1shf	A	517	574	1.7e-12	0.34	0.76		PHOSPHOTRANSFERASE FYN PROTO-ONCOGENE TYROSINE KINASE (E.C.2.7.1.112) 1SHF 3 (SH3 DOMAIN) 1SHF 4	
1180	4hck		518	575	1.1e-12	-0.11	0.63		HEMATOPOIETIC CELL KINASE; CHAIN: NULL;	TRANSFERASE HCK; SH3, PROTEIN TYROSINE KINASE, SIGNAL TRANSDUCTION, 2 TRANSFERASE
1185	1bih	A	1428	1819	5.1e-35			105.23	HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
1185	1bih	A	1536	1951	1.7e-46	-0.34	0.04		HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
1185	1bih	A	252	586	5.1e-32	-0.28	0.10		HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
1185	1cs6	A	1413	1621	1.7e-25	0.20	0.06		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1185	1cs6	A	211	595	1.4e-35	-0.11	0.52		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1185	1cs6	A	290	626	3.4e-36	-0.20	0.30		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1185	1cvs	C	1439	1620	3.4e-26	0.14	-0.05		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	CELL ADHESION GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1185	1cvs	C	255	381	5.1e-21	-0.30	0.52		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1185	1cvs	C	291	409	4e-15	-0.01	0.36		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1185	1cvs	D	1439	1620	3.4e-25	0.10	0.03		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH



Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1185	1cvs	D	1728	1951	1.5e-42	-0.17	0.07		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	FACTOR/GROWTH FACTOR RECEPTOR
1185	1cvs	D	255	381	8.5e-21	-0.29	0.24		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1185	1cvs	D	503	602	3.4e-14	0.05	0.40		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1185	1cvs	D	505	612	1.4e-17	0.26	0.30		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1185	1epf	A	1485	1622	3.4e-20	0.11	0.15		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1185	1epf	A	1730	1952	4e-27	0.15	0.27		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
1185	1epf	A	298	471	1.7e-22	0.10	0.60		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
1185	1epf	A	504	597	1e-15	0.44	0.18		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
1185	1ev2	E	1443	1620	3.4e-21	0.15	-0.09		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1185	1ev2	E	1527	1634	4e-15	-0.01	0.01		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1185	1ev2	E	291	396	2e-16	0.19	0.40		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2;

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2; SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1185	1ev2	G	1443	1624	1.7e-24	0.19	0.39		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2; SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1185	1ev2	G	1728	1951	8.5e-41	-0.16	0.16		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2; SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1185	1ev2	G	233	385	6.8e-20	-0.46	0.23		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2; SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1185	1evt	C	1439	1620	3.4e-24	0.24	-0.06		FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF1; FGFR1; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1185	1evt	C	255	381	1.2e-19	-0.29	0.11		FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1185	1f2q	A	291	386	6e-08	0.15	-0.05		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR1; FGFR1; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1185	1fhg	A	1528	1620	5.1e-20	0.58	0.80		TELOKIN; CHAIN: A	IMMUNE SYSTEM FC-EPSILON RI-ALPHA; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN
1185	1fhg	A	1721	1819	3.4e-24	0.04	1.00		TELOKIN; CHAIN: A	CONTRACTILE PROTEIN IMMUNOGLOBULIN FOLD, BETA BARREL
1185	1fhg	A	1854	1951	6.8e-24	0.41	0.87		TELOKIN; CHAIN: A	CONTRACTILE PROTEIN IMMUNOGLOBULIN FOLD, BETA BARREL
1185	1fhg	A	284	382	1.7e-22	0.60	1.00		TELOKIN; CHAIN: A	CONTRACTILE PROTEIN IMMUNOGLOBULIN FOLD, BETA BARREL
1185	1fhg	A	498	591	1e-20	0.15	0.55		TELOKIN; CHAIN: A	CONTRACTILE PROTEIN IMMUNOGLOBULIN FOLD, BETA BARREL
1185	1fhg	A	503	599	4e-21	0.35	1.00		TELOKIN; CHAIN: A	CONTRACTILE PROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										IMMUNOGLOBULIN FOLD, BETA BARREL
1185	1hng	A	297	386	6e-10	0.12	-0.14		T LYMPHOCYTE ADHESION GLYCOPROTEIN CD2 (RAT) IHNG 3	
1185	1hng	A	509	596	2e-14	0.10	-0.15		T LYMPHOCYTE ADHESION GLYCOPROTEIN CD2 (RAT) IHNG 3	
1185	1itb	B	1719	1950	1e-21	-0.28	0.00		INTERLEUKIN-1 BETA; CHAIN: A; TYPE 1 INTERLEUKIN-1 RECEPTOR; CHAIN: B;	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, RECEPTOR, 2 SIGNAL, COMPLEX (IMMUNOGLOBULIN/RECEPTOR)
1185	1itb	B	305	600	1.2e-22	-0.53	0.09		INTERLEUKIN-1 BETA; CHAIN: A; TYPE 1 INTERLEUKIN-1 RECEPTOR; CHAIN: B;	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, RECEPTOR, 2 SIGNAL, COMPLEX (IMMUNOGLOBULIN/RECEPTOR)
1185	1itb	B	322	590	5.1e-18	-0.42	0.03		INTERLEUKIN-1 BETA; CHAIN: A; TYPE 1 INTERLEUKIN-1 RECEPTOR; CHAIN: B;	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										RECEPTOR, 2 SIGNAL, COMPLEX (IMMUNOGLOBULIN/RECEPTOR)
1185	1koa		1533	1620	1.2e-15	0.59	0.59		TWITCHIN; CHAIN: NULL;	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION
1185	1koa		1725	1818	3.4e-17	0.37	0.52		TWITCHIN; CHAIN: NULL;	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION
1185	1koa		1859	1952	3.4e-18	0.97	0.90		TWITCHIN; CHAIN: NULL;	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION
1185	1koa		293	387	6.8e-15	0.44	0.90		TWITCHIN; CHAIN: NULL;	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION
1185	1koa		500	590	8.5e-16	0.36	0.77		TWITCHIN; CHAIN: NULL;	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION
1185	1mco	H	1524	1927	3.4e-12			110.47	IMMUNOGLOBULIN (MCG) WITH A HINGE DELETION IMCO 3	
1185	1mco	H	1542	1934	3.4e-12	-0.48	0.04		IMMUNOGLOBULIN (MCG) WITH A HINGE DELETION IMCO 3	
1185	1nct		1530	1620	4e-20	0.35	0.55		TITIN; CHAIN: NULL;	MUSCLE PROTEIN CONNECTIN, NEXTM5; CELL ADHESION, GLYCOPROTEIN, TRANSMEMBRANE, REPEAT, BRAIN, 2 IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3 MUSCLE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1185	1nct		1533	1621	3.4e-16	0.53	0.28		TITIN; CHAIN: NULL;	PROTEIN MUSCLE PROTEIN CONNECTIN, NEXTM5; CELL ADHESION, GLYCOPROTEIN, TRANSMEMBRANE, REPEAT, BRAIN, 2 IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3 MUSCLE PROTEIN
1185	1nct		1722	1817	2e-20	-0.10	0.40		TITIN; CHAIN: NULL;	MUSCLE PROTEIN CONNECTIN, NEXTM5; CELL ADHESION, GLYCOPROTEIN, TRANSMEMBRANE, REPEAT, BRAIN, 2 IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3 MUSCLE PROTEIN
1185	1nct		1729	1819	5.1e-19	0.21	0.16		TITIN; CHAIN: NULL;	MUSCLE PROTEIN CONNECTIN, NEXTM5; CELL ADHESION, GLYCOPROTEIN, TRANSMEMBRANE, REPEAT, BRAIN, 2 IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3 MUSCLE PROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1185	1nct		1858	1950	6e-22	0.20	0.51		TITIN; CHAIN: NULL;	MUSCLE PROTEIN CONNECTIN, NEXTM5; CELL ADHESION, GLYCOPROTEIN, TRANSMEMBRANE, REPEAT, BRAIN, 2 IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3 MUSCLE PROTEIN
1185	1nct		1863	1951	5.1e-18	0.51	0.25		TITIN; CHAIN: NULL;	MUSCLE PROTEIN CONNECTIN, NEXTM5; CELL ADHESION, GLYCOPROTEIN, TRANSMEMBRANE, REPEAT, BRAIN, 2 IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3 MUSCLE PROTEIN
1185	1nct		291	382	1.2e-19	0.54	1.00		TITIN; CHAIN: NULL;	MUSCLE PROTEIN CONNECTIN, NEXTM5; CELL ADHESION, GLYCOPROTEIN, TRANSMEMBRANE, REPEAT, BRAIN, 2 IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3 MUSCLE PROTEIN
1185	1nct		293	382	1e-18	0.41	0.99		TITIN; CHAIN: NULL;	MUSCLE PROTEIN



Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										CONNECTIN, NEXTM5; CELL ADHESION, GLYCOPROTEIN, TRANSMEMBRANE, REPEAT, BRAIN, 2 IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3 MUSCLE PROTEIN
1185	1nct		503	597	4e-22	0.02	0.99		TITIN; CHAIN: NULL;	MUSCLE PROTEIN CONNECTIN, NEXTM5; CELL ADHESION, GLYCOPROTEIN, TRANSMEMBRANE, REPEAT, BRAIN, 2 IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3 MUSCLE PROTEIN
1185	1nct		509	595	3.4e-18	0.51	0.99		TITIN; CHAIN: NULL;	MUSCLE PROTEIN CONNECTIN, NEXTM5; CELL ADHESION, GLYCOPROTEIN, TRANSMEMBRANE, REPEAT, BRAIN, 2 IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3 MUSCLE PROTEIN
1185	1tit		1531	1614	6e-17	0.64	0.65		TITIN, I27; CHAIN: NULL;	IMMUNOGLOBULIN-LIKE DOMAIN CONNECTIN I27,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										TITIN IG REPEAT 27; MUSCLE PROTEIN, IMMUNOGLOBULIN-LIKE DOMAIN
1185	1tit		1728	1810	1.2e-17	0.20	0.21		TITIN, I27; CHAIN: NULL;	IMMUNOGLOBULIN-LIKE DOMAIN CONNECTIN I27, TITIN IG REPEAT 27; MUSCLE PROTEIN, IMMUNOGLOBULIN-LIKE DOMAIN
1185	1tit		1862	1949	8e-19	0.64	0.03		TITIN, I27; CHAIN: NULL;	IMMUNOGLOBULIN-LIKE DOMAIN CONNECTIN I27, TITIN IG REPEAT 27; MUSCLE PROTEIN, IMMUNOGLOBULIN-LIKE DOMAIN
1185	1tit		506	594	1.2e-18	0.13	0.03		TITIN, I27; CHAIN: NULL;	IMMUNOGLOBULIN-LIKE DOMAIN CONNECTIN I27, TITIN IG REPEAT 27; MUSCLE PROTEIN, IMMUNOGLOBULIN-LIKE DOMAIN
1185	1tnm		1533	1620	1.8e-18	0.53	0.75		MUSCLE PROTEIN TITIN MODULE M5 (CONNECTIN) 1TNM 3 (NMR, MINIMIZED AVERAGE STRUCTURE) 1TNM 4 1TNM 58	
1185	1tnm		1533	1621	3.4e-16	0.57	0.52		MUSCLE PROTEIN TITIN MODULE M5 (CONNECTIN) 1TNM 3 (NMR, MINIMIZED AVERAGE STRUCTURE) 1TNM 4	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1185	1tnm		1729	1819	5.1e-19	0.40	0.34		1TNM 58 MUSCLE PROTEIN TITIN MODULE M5 (CONNECTIN) 1TNM 3 (NMR, MINIMIZED AVERAGE STRUCTURE) 1TNM 4 1TNM 58	
1185	1tnm		1863	1950	1e-20	0.62	0.82		MUSCLE PROTEIN TITIN MODULE M5 (CONNECTIN) 1TNM 3 (NMR, MINIMIZED AVERAGE STRUCTURE) 1TNM 4 1TNM 58	
1185	1tnm		293	382	1e-18	0.40	0.93		MUSCLE PROTEIN TITIN MODULE M5 (CONNECTIN) 1TNM 3 (NMR, MINIMIZED AVERAGE STRUCTURE) 1TNM 4 1TNM 58	
1185	1tnm		509	595	3.4e-18	0.53	1.00		MUSCLE PROTEIN TITIN MODULE M5 (CONNECTIN) 1TNM 3 (NMR, MINIMIZED AVERAGE STRUCTURE) 1TNM 4 1TNM 58	
1185	1tnm		513	597	4e-21	0.09	1.00		MUSCLE PROTEIN TITIN MODULE M5 (CONNECTIN) 1TNM 3 (NMR, MINIMIZED AVERAGE STRUCTURE) 1TNM 4 1TNM 58	
1185	1wit		1529	1620	6e-21	0.18	0.04		TWITCHIN 18TH IGSF MODULE; CHAIN: NULL;	MUSCLE PROTEIN IMMUNOGLOBULIN SUPERFAMILY, I SET, MUSCLE PROTEIN
1185	1wit		1861	1950	4e-22	0.55	-0.09		TWITCHIN 18TH IGSF MODULE;	MUSCLE PROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									CHAIN: NULL;	IMMUNOGLOBULIN SUPERFAMILY, I SET, MUSCLE PROTEIN
1185	1wit		291	381	8e-20	0.30	0.31		TWITCHIN 18TH IGSF MODULE; CHAIN: NULL;	MUSCLE PROTEIN
1185	1wit		505	597	6e-22	0.17	0.49		TWITCHIN 18TH IGSF MODULE; CHAIN: NULL;	IMMUNOGLOBULIN SUPERFAMILY, I SET, MUSCLE PROTEIN
1185	1wvb	X	1554	1621	1e-11	0.36	-0.03		BRAIN DERIVED NEUROTROPHIC FACTOR RECEPTOR TRKB; CHAIN: X;	TRANSFERASE TRK RECEPTOR, RECEPTOR TYROSINE KINASE, 3D-DOMAIN SWAPPING, 2 TRANSFERASE
1185	1wvb	X	291	388	2e-11	0.12	-0.09		BRAIN DERIVED NEUROTROPHIC FACTOR RECEPTOR TRKB; CHAIN: X;	TRANSFERASE TRK RECEPTOR, RECEPTOR TYROSINE KINASE, 3D-DOMAIN SWAPPING, 2 TRANSFERASE
1185	1wvc	A	1858	1950	4e-20	0.01	-0.14		NT-3 GROWTH FACTOR RECEPTOR TRKC; CHAIN: A;	TRANSFERASE TRK RECEPTOR, RECEPTOR TYROSINE KINASE, 3D-DOMAIN SWAPPING, 2 TRANSFERASE
1185	1wvc	A	503	597	2e-17	0.09	0.54		NT-3 GROWTH FACTOR RECEPTOR TRKC; CHAIN: A;	TRANSFERASE TRK RECEPTOR, RECEPTOR TYROSINE KINASE, 3D-DOMAIN SWAPPING, 2 TRANSFERASE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1185	1www	X	1534	1621	1.4e-14	0.11	0.04		NERVE GROWTH FACTOR; CHAIN: V, W; TRKA RECEPTOR; CHAIN: X, Y;	NERVE GROWTH FACTOR/TRKA COMPLEX BETA-NGF; COMPLEX, TRKA RECEPTOR, NERVE GROWTH FACTOR, CYSTEINE KNOT, 2 IMMUNOGLOBULIN LIKE DOMAIN, NERVE GROWTH FACTOR/TRKA COMPLEX
1185	1www	X	511	597	1e-16	0.16	0.00		NERVE GROWTH FACTOR; CHAIN: V, W; TRKA RECEPTOR; CHAIN: X, Y;	NERVE GROWTH FACTOR/TRKA COMPLEX BETA-NGF; COMPLEX, TRKA RECEPTOR, NERVE GROWTH FACTOR, CYSTEINE KNOT, 2 IMMUNOGLOBULIN LIKE DOMAIN, NERVE GROWTH FACTOR/TRKA COMPLEX
1185	1zxq		1471	1612	6e-12	-0.21	0.00		INTERCELLULAR ADHESION MOLECULE-2; CHAIN: NULL;	CELL ADHESION ICAM-2; IMMUNOGLOBULIN FOLD, CELL ADHESION, GLYCOPROTEIN, 2 TRANSMEMBRANE, REPEAT, SIGNAL
1185	2ncm		1530	1614	8e-16	0.00	-0.14		NEURAL CELL ADHESION MOLECULE; CHAIN: NULL;	CELL ADHESION NCAM DOMAIN 1; CELL ADHESION, GLYCOPROTEIN, HEPARIN-BINDING, GPI-ANCHOR, 2 NEURAL ADHESION MOLECULE,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1185	2ncm		1861	1948	4e-19	-0.01	0.03		NEURAL CELL ADHESION MOLECULE; CHAIN: NULL;	IMMUNOGLOBULIN FOLD, SIGNAL CELL ADHESION NCAM DOMAIN 1; CELL ADHESION, GLYCOPROTEIN, HEPARIN-BINDING, GPI-ANCHOR, 2 NEURAL ADHESION MOLECULE, IMMUNOGLOBULIN FOLD, SIGNAL
1185	2ncm		505	596	1.4e-17	0.02	0.31		NEURAL CELL ADHESION MOLECULE; CHAIN: NULL;	CELL ADHESION NCAM DOMAIN 1; CELL ADHESION, GLYCOPROTEIN, HEPARIN-BINDING, GPI-ANCHOR, 2 NEURAL ADHESION MOLECULE, IMMUNOGLOBULIN FOLD, SIGNAL
1185	3ncm	A	1530	1622	5.1e-13	0.36	0.62		NEURAL CELL ADHESION MOLECULE, LARGE ISOFORM; CHAIN: A;	CELL ADHESION PROTEIN NCAM MODULE 2; CELL ADHESION, GLYCOPROTEIN, HEPARIN-BINDING, GPI-ANCHOR, 2 NEURAL ADHESION MOLECULE, IMMUNOGLOBULIN FOLD, HOMOPHILIC 3 BINDING, CELL ADHESION PROTEIN
1185	3ncm	A	1531	1620	1.4e-17	0.06	0.78		NEURAL CELL ADHESION	CELL ADHESION PROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									MOLECULE, LARGE ISOFORM; CHAIN: A;	NCAM MODULE 2; CELL ADHESION, GLYCOPROTEIN, HEPARIN-BINDING, GPI-ANCHOR, 2 NEURAL ADHESION MOLECULE, IMMUNOGLOBULIN FOLD, HOMOPHILIC 3 BINDING, CELL ADHESION PROTEIN
1185	3ncm	A	1728	1817	1.4e-17	-0.13	0.04		NEURAL CELL ADHESION MOLECULE, LARGE ISOFORM; CHAIN: A;	CELL ADHESION PROTEIN NCAM MODULE 2; CELL ADHESION, GLYCOPROTEIN, HEPARIN-BINDING, GPI-ANCHOR, 2 NEURAL ADHESION MOLECULE, IMMUNOGLOBULIN FOLD, HOMOPHILIC 3 BINDING, CELL ADHESION PROTEIN
1185	3ncm	A	1862	1952	1.6e-20	0.29	0.31		NEURAL CELL ADHESION MOLECULE, LARGE ISOFORM; CHAIN: A;	CELL ADHESION PROTEIN NCAM MODULE 2; CELL ADHESION, GLYCOPROTEIN, HEPARIN-BINDING, GPI-ANCHOR, 2 NEURAL ADHESION MOLECULE, IMMUNOGLOBULIN FOLD, HOMOPHILIC 3 BINDING, CELL ADHESION PROTEIN
1185	3ncm	A	292	381	8e-18	0.23	0.64		NEURAL CELL ADHESION MOLECULE, LARGE ISOFORM;	CELL ADHESION PROTEIN NCAM MODULE 2; CELL

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									CHAIN: A;	ADHESION, GLYCOPROTEIN, HEPARIN-BINDING, GPI-ANCHOR, 2 NEURAL ADHESION MOLECULE, IMMUNOGLOBULIN FOLD, HOMOPHILIC 3 BINDING, CELL ADHESION PROTEIN
1185	3ncm	A	506	597	8e-20	0.54	0.28		NEURAL CELL ADHESION MOLECULE, LARGE ISOFORM; CHAIN: A;	CELL ADHESION PROTEIN NCAM MODULE 2; CELL ADHESION, GLYCOPROTEIN, HEPARIN-BINDING, GPI-ANCHOR, 2 NEURAL ADHESION MOLECULE, IMMUNOGLOBULIN FOLD, HOMOPHILIC 3 BINDING, CELL ADHESION PROTEIN
1185	8fab	A	297	487	1.5e-08	-0.25	0.09		IMMUNOGLOBULIN FAB FRAGMENT FROM HUMAN IMMUNOGLOBULIN IGG1 (LAMBD A, HIL) 8FAB 3	
1197	1cfl	A	1	336	1.5e-48			50.36	ARRESTIN; CHAIN: A, B, C, D;	STRUCTURAL PROTEIN RETINAL S-ANTIGEN, 48 KD PROTEIN; VISUAL ARRESTIN, DESENSITISATION OF THE VISUAL TRANSDUCTION 2 CASCADE, BINDING TO ACTIVATED AND



Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										PHOSPHORYLATED RHODOPSIN
1197	1cfl	A	16	241	1.5e-48	-0.03	0.22		ARRESTIN; CHAIN: A, B, C, D;	STRUCTURAL PROTEIN RETINAL S-ANTIGEN, 48 KD PROTEIN; VISUAL ARRESTIN, DESENSITISATION OF THE VISUAL TRANSDUCTION 2 CASCADE, BINDING TO ACTICATED AND PHOSPHORYLATED RHODOPSIN
1197	1cfl	D	1	336	1.5e-48			52.32	ARRESTIN; CHAIN: A, B, C, D;	STRUCTURAL PROTEIN RETINAL S-ANTIGEN, 48 KD PROTEIN; VISUAL ARRESTIN, DESENSITISATION OF THE VISUAL TRANSDUCTION 2 CASCADE, BINDING TO ACTICATED AND PHOSPHORYLATED RHODOPSIN
1197	1cfl	D	16	241	1.5e-48	0.16	0.29		ARRESTIN; CHAIN: A, B, C, D;	STRUCTURAL PROTEIN RETINAL S-ANTIGEN, 48 KD PROTEIN; VISUAL ARRESTIN, DESENSITISATION OF THE VISUAL TRANSDUCTION 2 CASCADE, BINDING TO ACTICATED AND PHOSPHORYLATED

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										RHODOPSIN
1202	1fs1	A	674	709	8.4e-05	-0.42	0.76		CYCLIN A/CDK2-ASSOCIATED P19; CHAIN: A, C; CYCLIN A/CDK2-ASSOCIATED P45; CHAIN: B, D;	LIGASE SKP2 F-BOX; SKP1; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
1214	1awe		247	343	1.2e-05	0.19	0.01		SOS1; CHAIN: NULL;	SIGNAL TRANSDUCTION SIGNAL TRANSDUCTION, SOS, PLECKSTRIN HOMOLOGY (PH) DOMAIN
1214	1bak		255	369	1e-10	0.04	-0.08		G-PROTEIN COUPLED RECEPTOR KINASE 2; CHAIN: NULL;	TRANSFERASE GRK-2, BETA-ADRENERGIC RECEPTOR KINASE 1, BETA-ARK PLECKSTRIN HOMOLOGY DOMAIN, PH DOMAIN, SIGNAL TRANSDUCTION, 2 G-BETA-GAMMA BINDING DOMAIN, BETA-ADRENERGIC RECEPTOR 3 KINASE, BETA-ARK, G-PROTEIN COUPLED RECEPTOR KINASE (GRK-2)
1214	1bc9		56	255	1.1e-87			294.37	CYTOHESIN-1; CHAIN: NULL;	EXCHANGE FACTOR B2-1, SEC7 HOMOLOG B2-1; EXCHANGE FACTOR, INTEGRIN BINDING PROTEIN
1214	1bc9		57	247	1.1e-87	0.69	1.00		CYTOHESIN-1; CHAIN: NULL;	EXCHANGE FACTOR B2-1,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										SEC7 HOMOLOG B2-1; EXCHANGE FACTOR, INTEGRIN BINDING PROTEIN
1214	1bc9		57	250	8.5e-50	0.81	1.00		CYTOHESIN-1; CHAIN: NULL;	EXCHANGE FACTOR B2-1, SEC7 HOMOLOG B2-1; EXCHANGE FACTOR, INTEGRIN BINDING PROTEIN
1214	1dbh	A	33	343	6.8e-18	-0.24	0.10		HUMAN SOS 1; CHAIN: A;	GENE REGULATION SON OF SEVENLESS PROTEIN; GUANINE NUCLEOTIDE EXCHANGE FACTOR, GENE REGULATION
1214	1fgy	A	256	355	4.8e-35	0.35	1.00		GRP1; CHAIN: A;	SIGNALING PROTEIN ARF1 GUANINE NUCLEOTIDE EXCHANGE FACTOR AND PH DOMAIN
1214	1fgy	A	265	354	1.7e-19	0.01	1.00		GRP1; CHAIN: A;	SIGNALING PROTEIN ARF1 GUANINE NUCLEOTIDE EXCHANGE FACTOR AND PH DOMAIN
1214	1pbv		52	246	3.6e-91			319.44	ARNO; CHAIN: NULL;	EXCHANGE FACTOR ARF NUCLEOTIDE-BINDING SITE OPENER; EXCHANGE FACTOR, SEC7, ARNO, ARF FUNCTIONAL CLASS: GUANINE 2 NUCLEOTIDE EXCHANGE FACTOR
1214	1pbv		52	246	3.6e-91	1.00	1.00		ARNO; CHAIN: NULL;	EXCHANGE FACTOR ARF NUCLEOTIDE-BINDING SITE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1214	1pbv		56	246	5.1e-48	1.05	1.00		ARNO; CHAIN: NULL;	OPENER; EXCHANGE FACTOR, SEC7, ARNO, ARF FUNCTIONAL CLASS: GUANINE 2 NUCLEOTIDE EXCHANGE FACTOR
1214	1pms		247	343	8.5e-06	0.14	0.51		SOS 1; CHAIN: NULL;	EXCHANGE FACTOR ARF NUCLEOTIDE-BINDING SITE OPENER; EXCHANGE FACTOR, SEC7, ARNO, ARF FUNCTIONAL CLASS: GUANINE 2 NUCLEOTIDE EXCHANGE FACTOR
1217	1ez3	A	12	148	0.0004	0.06	0.39		SYNTAXIN-1A; CHAIN: A, B, C;	SIGNAL TRANSDUCTION SON OF SEVENLESS; PLECKSTRIN, SON OF SEVENLESS, SIGNAL TRANSDUCTION
1226	1gof		52	250	6.8e-13	0.18	-0.01		OXIDOREDUCTASE(OXYGEN(A) ) GALACTOSE OXIDASE (E.C.1.1.3.9) (PH 4.5) 1GOF 3	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE
1227	1gof		11	274	3.4e-13	-0.03	0.42		OXIDOREDUCTASE(OXYGEN(A) ) GALACTOSE OXIDASE (E.C.1.1.3.9) (PH 4.5) 1GOF 3	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1231	1a17		86	256	1.2e-07	0.25	0.24		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRATRICPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN- PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE
1231	1e96	B	1	129	1.2e-08	-0.25	0.30		RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1; CHAIN: A; NEUTROPHIL CYTOSOL FACTOR 2 (NCF-2) CHAIN: B;	SIGNALLING COMPLEX RAC1; P67PHOX; SIGNALLING COMPLEX, GTPASE, NADPH OXIDASE, PROTEIN-PROTEIN 2 COMPLEX, TPR MOTIF
1231	1e96	B	224	378	5.1e-13	-0.00	-0.15		RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1; CHAIN: A; NEUTROPHIL CYTOSOL FACTOR 2 (NCF-2) CHAIN: B;	SIGNALLING COMPLEX RAC1; P67PHOX; SIGNALLING COMPLEX, GTPASE, NADPH OXIDASE, PROTEIN-PROTEIN 2 COMPLEX, TPR MOTIF
1231	1e96	B	37	188	1.7e-14	0.06	-0.09		RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1; CHAIN: A; NEUTROPHIL CYTOSOL FACTOR 2 (NCF-2) CHAIN: B;	SIGNALLING COMPLEX RAC1; P67PHOX; SIGNALLING COMPLEX, GTPASE, NADPH OXIDASE, PROTEIN-PROTEIN 2 COMPLEX, TPR MOTIF
1231	1e1r	A	32	150	3.4e-22	0.37	0.34		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR- DOMAIN, PEPTIDE- COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1231	1elw	A	32	141	8.5e-20	0.26	0.60		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1231	1elw	A	4	115	1.7e-08	0.28	0.04		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1231	1elw	A	71	196	5.1e-09	0.05	-0.14		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1231	1fch	A	15	120	5.1e-09	-0.00	-0.17		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	SIGNALING PROTEIN PEROXISOMORE RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
1231	1fch	A	38	309	1.7e-37	0.19	-0.06		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	SIGNALING PROTEIN PEROXISOMORE RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1248	1c4o	A	76	253	5.1e-21	0.42	0.89		DNA NUCLEOTIDE EXCISION REPAIR ENZYME UVRB; CHAIN: A;	REPLICATION DNA NUCLEOTIDE EXCISION REPAIR, UVRABC, HELICASE, 2 HYPERTHERMOSTABLE PROTEIN
1248	1d2m	A	76	256	3.4e-21	0.40	0.71		EXCINUCLEASE ABC SUBUNIT B; CHAIN: A;	HYDROLASE UVRB; MULTIDOMAIN PROTEIN
1248	1d9x	A	22	272	1e-24	-0.25	0.43		EXCINUCLEASE UVRABC COMPONENT UVRB; CHAIN: A;	GENE REGULATION APO PROTEIN
1248	1fuk	A	104	258	1.7e-43	0.58	1.00		EUKARYOTIC INITIATION FACTOR 4A; CHAIN: A;	TRANSLATION YEAST INITIATION FACTOR 4A, EIF4A; HELICASE, INITIATION FACTOR 4A, DEAD-BOX PROTEIN
1248	1fuu	B	7	258	5.1e-66	0.04	0.84		YEAST INITIATION FACTOR 4A; CHAIN: A, B;	TRANSLATION EUKARYOTIC INITIATION FACTOR 4A; IF4A, HELICASE, DEAD-BOX PROTEIN
1253	1a25	A	983	1123	3.4e-48	0.08	1.00		PROTEIN KINASE C (BETA); CHAIN: A, B;	CALCIUM-BINDING PROTEIN CALB; CALCIUM++/PHOSPHOLIPID BINDING PROTEIN, 2 CALCIUM-BINDING PROTEIN
1253	1b8q	A	800	871	1.2e-15	0.99	0.99		NEURONAL NITRIC OXIDE SYNTHASE; CHAIN: A; HEPTAPEPTIDE; CHAIN: B;	OXIDOREDUCTASE PDZ DOMAIN, NNOS, NITRIC OXIDE SYNTHASE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1253	1be9	A	828	890	9.6e-11	-0.05	0.72		PSD-95; CHAIN: A; CRIP1; CHAIN: B;	PEPTIDE RECOGNITION PEPTIDE RECOGNITION, PROTEIN LOCALIZATION
1253	1byn	A	983	1119	6.8e-50	0.14	1.00		SYNAPTOTAGMIN I; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN, C2-DOMAIN, EXOCYTOSIS, NEUROTRANSMITTER 2 RELEASE, ENDOCYTOSIS/EXOCYTOSIS
1253	1cjt	A	994	1126	9.6e-26	0.05	0.09		CYTOSOLIC PHOSPHOLIPASE A2; CHAIN: A, B;	HYDROLASE CPLA2; PHOSPHOLIPASE, LIPID-BINDING, HYDROLASE
1253	1djt	B	999	1119	8.4e-21	0.21	0.87		PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B;	LIPID DEGRADATION PLC-D1; PHOSPHORIC DIESTER HYDROLASE, HYDROLASE, 2 LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3 PHOSPHOINOSITIDE-SPECIFIC
1253	1dqv	A	981	1121	3.4e-21	0.02	0.49		SYNAPTOTAGMIN III; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS BETA SANDWICH, CALCIUM ION, C2 DOMAIN
1253	1dqv	A	982	1125	1.5e-43	0.45	1.00		SYNAPTOTAGMIN III; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS BETA SANDWICH, CALCIUM ION, C2 DOMAIN
1253	1dsy	A	982	1124	1.7e-52	0.14	1.00		PROTEIN KINASE C, ALPHA TYPE; CHAIN: A;	TRANSFERASE CALCIUM++, PHOSPHOLIPID BINDING PROTEIN, CALCIUM-BINDING 2 PROTEIN,



Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1253	1i16		800	876	1.1e-16	0.59	0.92		INTERLEUKIN 16; CHAIN: NULL;	PHOSPHATIDYL SERINE, PROTEIN KINASE C
1253	1pdr		800	860	4.8e-13	0.30	0.09		HUMAN DISCS LARGE PROTEIN; CHAIN: NULL;	LYMPHOCYTE CHEMOATTRACTANT FACTOR, PDZ DOMAIN
1253	1qau	A	799	898	4.8e-16	0.12	0.34		NEURONAL NITRIC OXIDE SYNTHASE (RESIDUES 1-130); CHAIN: A;	SIGNAL TRANSDUCTION HDLG, DHR3 DOMAIN; SIGNAL TRANSDUCTION, SH3 DOMAIN, REPEAT
1253	1rsy		983	1117	1.7e-49	0.01	1.00		CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN 1 (FIRST C2 DOMAIN) (CALB) IRSY 3	OXIDOREDUCTASE BETA-FINGER
1253	3rpb	A	985	1122	1.2e-26	0.24	0.99		RABPHILIN 3-A; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS C2-DOMAINS, C2B-DOMAIN, RABPHILIN, ENDOCYTOSIS/EXOCYTOSIS S
1253	3rpb	A	986	1119	4.8e-29	0.19	1.00		RABPHILIN 3-A; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS C2-DOMAINS, C2B-DOMAIN, RABPHILIN, ENDOCYTOSIS/EXOCYTOSIS S
1254	1a25	A	983	1114	5.1e-51	0.11	1.00		PROTEIN KINASE C (BETA); CHAIN: A, B;	CALCIUM-BINDING PROTEIN CALB; CALCIUM++/PHOSPHOLIPID

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										BINDING PROTEIN, 2 CALCIUM-BINDING PROTEIN
1254	1a25	A	983	1117	5.1e-51			94.21	PROTEIN KINASE C (BETA); CHAIN: A, B;	CALCIUM-BINDING PROTEIN CALB; CALCIUM++/PHOSPHOLIPID BINDING PROTEIN, 2 CALCIUM-BINDING PROTEIN
1254	1b8q	A	800	871	1.2e-15	0.99	0.99		NEURONAL NITRIC OXIDE SYNTHASE; CHAIN: A; HEPTAPEPTIDE; CHAIN: B;	OXIDOREDUCTASE PDZ DOMAIN, NNOS, NITRIC OXIDE SYNTHASE
1254	1be9	A	828	890	9.6e-11	-0.05	0.72		PSD-95; CHAIN: A; CRIP1; CHAIN: B;	PEPTIDE RECOGNITION PEPTIDE RECOGNITION, PROTEIN LOCALIZATION
1254	1byn	A	983	1110	1.5e-52	0.40	1.00		SYNAPTOTAGMIN I; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN, C2-DOMAIN, EXOCYTOSIS, NEUROTRANSMITTER 2 RELEASE, ENDOCYTOSIS/EXOCYTOSIS
1254	1c1y	A	994	1117	1.2e-26	0.02	0.17		CYTOSOLIC PHOSPHOLIPASE A2; CHAIN: A, B;	HYDROLASE CPLA2; PHOSPHOLIPASE, LIPID-BINDING, HYDROLASE
1254	1d1x	B	999	1110	6e-23	0.23	0.81		PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B;	LIPID DEGRADATION PLC-D1; PHOSPHORIC DIESTER HYDROLASE, HYDROLASE, LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOLIPASE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										C, 3 PHOSPHONOSITIDE-SPECIFIC
1254	1dqv	A	981	1109	1e-23	0.22	0.87		SYNAPTOTAGMIN III; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS BETA SANDWICH, CALCIUM ION, C2 DOMAIN
1254	1dqv	A	984	1116	6.8e-45	0.47	1.00		SYNAPTOTAGMIN III; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS BETA SANDWICH, CALCIUM ION, C2 DOMAIN
1254	1dsy	A	982	1115	1.7e-54	0.03	1.00		PROTEIN KINASE C, ALPHA TYPE; CHAIN: A;	TRANSFERASE CALCIUM <sup>++</sup> , PHOSPHOLIPID BINDING PROTEIN, CALCIUM-BINDING 2 PROTEIN, PHOSPHATIDYL SERINE, PROTEIN KINASE C
1254	1i16		800	876	1.1e-16	0.59	0.92		INTERLEUKIN 16; CHAIN: NULL;	CYTOKINE LCF; CYTOKINE, LYMPHOCYTE
1254	1pdr		800	860	4.8e-13	0.30	0.09		HUMAN DISCS LARGE PROTEIN; CHAIN: NULL;	CHEMOATTRACTANT FACTOR, PDZ DOMAIN
1254	1qau	A	799	898	4.8e-16	0.12	0.34		NEURONAL NITRIC OXIDE SYNTHASE (RESIDUES 1-130); CHAIN: A;	SIGNAL TRANSDUCTION HDLG, DHR3 DOMAIN; SIGNAL TRANSDUCTION, SH3 DOMAIN, REPEAT
1254	1rsy		983	1108	5.1e-52	0.53	1.00		CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) IRSY 3	OXIDOREDUCTASE BETA-FINGER
1254	3rpb	A	985	1113	1e-30	0.23	1.00		RABPHILIN 3-A; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS C2-DOMAINS, C2B-

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1254	3tpb	A	986	1110	3.6e-31	0.51	1.00		RABPHILIN 3-A; CHAIN: A;	DOMAIN, RABPHILIN, ENDOCYTOSIS/EXOCYTOSIS
										S
										ENDOCYTOSIS/EXOCYTOSIS C2-DOMAINS, C2B-DOMAIN, RABPHILIN, ENDOCYTOSIS/EXOCYTOSIS
1259	1clg	A	686	981	3.4e-26	-0.68	0.15		TROPOMYOSIN; CHAIN: A, B, C, D	CONTRACTILE PROTEIN TROPOMYOSIN COILED-COIL ALPHA-HELICAL, CONTRACTILE PROTEIN
1259	1cum	A	1345	1554	3.6e-19	0.10	-0.06		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1259	1cum	A	1377	1592	1.2e-15	0.11	-0.13		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1259	1cum	A	20	245	2.4e-18	0.09	0.54		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1259	1cun	A	255	471	9.6e-12	0.01	0.22		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1259	1cun	A	765	959	2.4e-09	0.17	-0.03		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1259	1cun	A	918	1118	9.6e-16	0.01	-0.07		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1259	1cun	A	97	321	3.6e-14	0.15	0.24		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1259	1dn1	B	1509	1729	1.2e-09	-0.05	0.23		SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
1259	1dn1	B	365	546	4.8e-13	-0.03	0.36		SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
1259	1dn1	B	382	582	1.2e-11	0.15	0.59		SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
1259	1fio	A	188	376	1.1e-07	0.14	0.49		SSO1 PROTEIN; CHAIN: A;	MEMBRANE PROTEIN FOUR HELIX BUNDLE, ALPHA HELIX
1259	1fio	A	765	964	2.4e-11	-0.08	0.00		SSO1 PROTEIN; CHAIN: A;	MEMBRANE PROTEIN FOUR HELIX BUNDLE, ALPHA HELIX
1259	1fxk	A	13	104	8.5e-08	0.10	0.06		PREFOLDIN; CHAIN: A; PREFOLDIN; CHAIN: B; PREFOLDIN; CHAIN: C;	CHAPERONE ARCHAEAL PROTEIN
1259	1quu	A	1447	1709	4.8e-19	-0.17	0.03		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
1259	1quu	A	172	472	3.6e-18	-0.38	0.07		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
1261	1a81	E	222	441	1.7e-18			59.55	SYK KINASE; CHAIN: A, C, E, G, I, K; T-CELL SURFACE GLYCOPROTEIN CD3 EPSILON CHAIN; CHAIN: B, D, F, H, J, L;	COMPLEX (TRANSFERASE/PEPTIDE) ITAM PEPTIDE; COMPLEX (TRANSFERASE/PEPTIDE);

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1261	1ab2		331	441	1.2e-23			59.80	TRANSFERASE(PHOSPHOTRANSFERASE) PROTO-ONCOGENE TYROSINE KINASE (E.C.2.7.1.112) 1AB2 3 (SRC HOMOLOG 2 DOMAIN) ("ABELSON", SH2 ABL) 1AB2 4 (NMR, 20 STRUCTURES) 1AB2 5	SYK, KINASE, SH2 DOMAIN, ITAM
1261	1ab2		339	438	1.2e-23	0.39	0.57		TRANSFERASE(PHOSPHOTRANSFERASE) PROTO-ONCOGENE TYROSINE KINASE (E.C.2.7.1.112) 1AB2 3 (SRC HOMOLOG 2 DOMAIN) ("ABELSON", SH2 ABL) 1AB2 4 (NMR, 20 STRUCTURES) 1AB2 5	
1261	1aya	A	339	436	7.2e-22	0.54	0.99		HYDROLASE(SH2 DOMAIN) TYROSINE PHOSPHATASE SYP (N-TERMINAL SH2 DOMAIN) 1AYA 3 (PTP1D, SHPTP2) (E.C.3.1.3.48) COMPLEXED WITH THE PEPTIDE 1AYA 4 PDGFR-1009 1AYA 5	
1261	1bfi		336	436	4.8e-22	0.22	0.96		P85 ALPHA; CHAIN: NULL;	SH2 DOMAIN PHOSPHATIDYLINOSITOL 3-KINASE REGULATORY ALPHA SH2 DOMAIN, P85ALPHA, PI 3-KINASE, NMR, C TERMINAL SH2 2 DOMAIN
1261	1d0s	A	5	193	2.4e-08	0.31	-0.15		NICOTINATE	TRANSFERASE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									MONONUCLEOTIDE:5,6- CHAIN: A;	DINUCLEOTIDE-BINDING MOTIF, PHOSPHORIBOSYL TRANSFERASE
1261	1fns		334	436	6e-22	0.21	1.00		GROWTH FACTOR RECEPTOR BOUND PROTEIN-2; CHAIN: NULL;	SH2 DOMAIN GRB2; GRB2, SH2 DOMAIN, PROTEIN NMR, SOLUTION STRUCTURES
1261	1fmk		281	432	5.1e-24	0.28	0.05		TYROSINE-PROTEIN KINASE SRC; CHAIN: NULL;	PHOSPHOTRANSFERASE C-SRC, P60-SRC; SRC, TYROSINE KINASE, PHOSPHORYLATION, SH2, SH3, 2 PHOSPHOTYROSINE, PROTO-ONCOGENE, PHOSPHOTRANSFERASE
1261	1lck	A	283	436	1.7e-22	0.16	0.48		P56=LCK= TYROSINE KINASE; 1LCK 7 CHAIN: A; 1LCK 8 TAIL PHOSHOPEPTIDE TEGQ(PHOSHO)YQPQPA; 1LCK 14 CHAIN: B; 1LCK 15	COMPLEX (KINASE/PEPTIDE)
1261	1osm	A	4	66	6e-08	1.24	-0.20		OMPK36; CHAIN: A, B, C;	OUTER MEMBRANE PROTEIN OSMOPORIN; OUTER MEMBRANE PROTEIN, NON-SPECIFIC PORIN, OSMOPORIN, 2 BETA-BARREL, TRANSMEMBRANE
1261	1pho		5	67	3.6e-08	1.98	-0.19		OUTER MEMBRANE PROTEIN PHOSPHOPORIN (PHOE) 1PHO 3	
1261	1qg1	E	338	436	9.6e-22	0.50	0.95		GROWTH FACTOR RECEPTOR BINDING PROTEIN; CHAIN: E; SHC-DERIVED PEPTIDE; CHAIN:	HORMONE/GROWTH FACTOR GRB2-SH2; SIGNAL TRANSDUCTION, SH2



Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									I;	DOMAIN, PHOSPHOTYROSYL PEPTIDE, 2 COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE), HORMONE/GROWTH FACTOR
1261	2abl		272	437	8.5e-28			64.01	ABL TYROSINE KINASE; CHAIN: NULL;	TRANSFERASE TRANSFERASE, TYROSINE KINASE, SH3, SH2, ONCOPROTEIN
1261	2abl		272	437	8.5e-28	0.01	0.19		ABL TYROSINE KINASE; CHAIN: NULL;	TRANSFERASE TRANSFERASE, TYROSINE KINASE, SH3, SH2, ONCOPROTEIN
1261	2pna		336	436	2.4e-23	0.20	0.90		SIGNALING PROTEIN PHOSPHATIDYLINOSITOL 3-KINASE (E.C.2.7.1.137) (N-TERMINAL 2PNA 3 SH2 DOMAIN OF P85-ALPHA SUBUNIT) (NMR, 22 STRUCTURES) 2PNA 4	
1263	1a17		285	350	9.6e-13	-0.35	0.60		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRATRICPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE
1263	1ejf	A	3	83	1.2e-05	0.33	0.86		PROGESTERONE RECEPTOR P23; CHAIN: A, B;	CHAPERONE CHAPERONE, CO-CHAPERONE, BETA-

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1263	1qqe	A	53	339	4.8e-11			73.19	VESICULAR TRANSPORT PROTEIN SEC17; CHAIN: A;	SANDWICH PROTEIN TRANSPORT HELIX-TURN-HELIX TPR- LIKE REPEAT, PROTEIN TRANSPORT
1263	1quu	A	93	190	2.4e-08	0.02	-0.19		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
1264	1qsa	A	280	501	4.8e-09	0.00	-0.20		SOLUBLE LYTIC TRANSGLYCOSYLASE SLT70; CHAIN: A;	TRANSFERASE ALPHA- SUPERHELIX, TRANSFERASE
1264	2trc	P	302	452	4.8e-10	0.13	-0.20		TRANSDUCIN; CHAIN: B, G; PHOSDUCIN; CHAIN: P;	COMPLEX (TRANSDUCER/TRANSDUCT ION) GT BETA-GAMMA; MEKA, PP33; PHOSDUCIN, TRANSDUCIN, BETA- GAMMA, SIGNAL TRANSDUCTION, 2 REGULATION, PHOSPHORYLATION, G PROTEINS, THIOREDOXIN, 3 VISION, MEKA, COMPLEX (TRANSDUCER/TRANSDUCT ION)
1268	1cun	A	227	417	1.2e-07	-0.31	0.24		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1268	1cun	A	374	595	2.4e-18	0.00	0.35		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1268	1cun	A	456	711	6e-12	-0.01	0.28		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1268	1quu	A	526	735	2.4e-14	0.01	-0.17		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
1268	1ses	A	320	391	0.0001	-0.26	0.04		LIGASE(SYNTHETASE) SERYL-TRNA SYNTHETASE (E.C.6.1.1.11) (SERINE-TRNA LIGASE) 1SES 3 COMPLEXED WITH SERYL-HYDROXAMATE-AMP 1SES 4	
1274	1av1	A	5	96	2.2e-09	0.10	-0.19		APOLIPOPROTEIN A-I; CHAIN: A, B, C, D;	LIPID TRANSPORT APO A-I; LIPOPROTEIN, LIPID TRANSPORT,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										CHOLESTEROL METABOLISM, 2 ATHEROSCLEROSIS, HDL, LCAT-ACTIVATION
1274	1cun	A	9	102	4.4e-09	0.17	-0.20		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1274	1quu	A	9	102	2.2e-10	0.18	-0.20		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
1277	1alh	A	302	405	1.4e-16	0.45	-0.19		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1277	1alh	A	382	460	8.5e-28	0.08	0.53		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1277	1alh	A	409	472	1.7e-23	0.10	0.30		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1277	1buo	A	20	142	2.2e-23			65.70	PROMYELOCYTIC LEUKEMIA ZINC FINGER PROTEIN PLZF; CHAIN: A;	GENE REGULATION POZ DOMAIN; PROTEIN-PROTEIN INTERACTION DOMAIN, TRANSCRIPTIONAL 2 REPRESSOR, ZINC-FINGER PROTEIN, X-RAY CRYSTALLOGRAPHY, 3 PROTEIN STRUCTURE, PROMYELOCYTIC LEUKEMIA, GENE REGULATION
1277	1buo	A	23	134	6.8e-21	0.06	1.00		PROMYELOCYTIC LEUKEMIA ZINC FINGER PROTEIN PLZF; CHAIN: A;	GENE REGULATION POZ DOMAIN; PROTEIN-PROTEIN INTERACTION DOMAIN, TRANSCRIPTIONAL 2 REPRESSOR, ZINC-FINGER PROTEIN, X-RAY CRYSTALLOGRAPHY, 3 PROTEIN STRUCTURE, PROMYELOCYTIC LEUKEMIA, GENE REGULATION
1277	1buo	A	23	142	2.2e-23	0.63	1.00		PROMYELOCYTIC LEUKEMIA ZINC FINGER PROTEIN PLZF; CHAIN: A;	GENE REGULATION POZ DOMAIN; PROTEIN-PROTEIN INTERACTION DOMAIN, TRANSCRIPTIONAL 2 REPRESSOR, ZINC-FINGER PROTEIN, X-RAY

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										CRYSTALLOGRAPHY, 3 PROTEIN STRUCTURE, PROMYELOCYTIC LEUKEMIA, GENE REGULATION
1277	1mey	C	250	349	8.5e-27	0.15	-0.19		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1277	1mey	C	301	405	6.8e-32	0.33	-0.18		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1277	1mey	C	381	460	6.8e-46	0.41	0.66		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1277	1mey	C	408	473	6.8e-39	-0.15	0.28		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1277	1mey	G	299	349	3.4e-09	0.73	-0.19		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	STRUCTURE, COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1277	1mey	G	379	405	1.2e-11	0.18	-0.13		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1277	1hf3	A	372	433	1.5e-15	0.21	-0.07		TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)
1277	1hf6	A	290	441	3.4e-23	0.43	0.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1277	1ff6	A	372	473	1.7e-25	0.14	0.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1277	1ubd	C	372	460	6.8e-27	0.33	0.21		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1277	1ubd	C	388	468	1.5e-26	-0.33	0.22		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1277	2adr		374	407	8.5e-09	0.57	-0.17		ADR1; CHAIN: NULL;	TRANSCRIPTION REGULATION



Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										TRANSCRIPTION REGULATION, ADR1, ZINC FINGER, NMR
1277	2gli	A	283	404	5.1e-19	0.31	-0.20		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1277	2gli	A	343	432	1.4e-23	0.22	-0.13		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1287	1a6q		72	445	8.5e-65			54.51	PHOSPHATASE 2C; CHAIN: NULL;	HYDROLASE CATALYTIC MECHANISM, METALLOENZYME, PROTEIN PHOSPHATASE 2C, 2 SIGNAL TRANSDUCTUIN, X-RAY CRYSTALLOGRAPHY, HYDROLASE
1287	1a6q		82	451	8.5e-65	-0.04	1.00		PHOSPHATASE 2C; CHAIN: NULL;	HYDROLASE CATALYTIC MECHANISM, METALLOENZYME, PROTEIN PHOSPHATASE 2C, 2 SIGNAL TRANSDUCTUIN, X-RAY CRYSTALLOGRAPHY, HYDROLASE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1291	1d0s	A	81	304	6e-08	0.11	-0.20		NICOTINATE MONONUCLEOTIDE:5,6- CHAIN: A;	TRANSFERASE DINUCLEOTIDE-BINDING MOTIF, PHOSPHORIBOSYL TRANSFERASE
1292	1cwv	A	7	501	2.2e-14			74.08	INVASIN; CHAIN: A;	STRUCTURAL PROTEIN INTEGRIN-BINDING PROTEIN, INV GENE
1293	1dvp	A	33	96	0.00017	-0.91	0.05		HEPATOCTYTE GROWTH FACTOR-REGULATED TYROSINE CHAIN: A;	TRANSFERASE HRS; HRS, VHS, FYVE, ZINC FINGER, SUPERHELIX
1293	1dvp	A	54	111	1.2e-05	-0.19	0.03		HEPATOCTYTE GROWTH FACTOR-REGULATED TYROSINE CHAIN: A;	TRANSFERASE HRS; HRS, VHS, FYVE, ZINC FINGER, SUPERHELIX
1293	1vfy	A	57	111	8e-06	-0.80	0.10		PHOSPHATIDYLINOSITOL-3-PHOSPHATE BINDING FYVE CHAIN: A;	TRANSPORT PROTEIN FYVE DOMAIN, ENDOSOME MATURATION, INTRACELLULAR TRAFFICKING, 2 TRANSPORT PROTEIN
1298	1cun	A	355	563	2.2e-09	-0.27	0.62		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1298	1cun	A	462	674	4.4e-13	-0.08	0.04		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1298	1quu	A	443	681	8.8e-24	-0.19	0.22		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1299	1awc	B	105	252	6.8e-43	0.27	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
1299	1awc	B	138	262	3.4e-34	0.18	0.96		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1299	1awc	B	34	187	6.8e-43			73.20	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1;

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA- BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1299	1awc	B	36	186	2.2e-38	0.56	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA- BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1299	1awc	B	38	186	1.4e-37	0.45	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA- BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1299	1awc	B	5	153	1.7e-36	0.10	0.92		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA- BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1299	1awc	B	72	219	8.5e-40	0.27	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1299	1bd8		108	255	5.1e-31	0.07	0.96		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1299	1bd8		36	190	6.6e-40			75.94	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1299	1bd8		38	187	1.3e-35	0.33	1.00		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1299	1bd8		67	221	6.6e-40	0.16	1.00		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1299	1bd8		75	219	3.4e-33	0.31	1.00		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1299	1bi7	B	102	221	6.6e-26	0.04	0.89		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; MULTIPLE TUMOR SUPPRESSOR; CHAIN: B;	COMPLEX (KINASE/ANTI-ONCOGENE) CDK6; P16INK4A, MTS1; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, MULTIPLE TUMOR SUPPRESSOR, 3 MTS1, COMPLEX (KINASE/ANTI-ONCOGENE) HEADER
1299	1blx	B	108	255	6.8e-31	0.02	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1299	1blx	B	36	192	1.1e-39	0.48	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1299	1blx	B	68	225	2.2e-39	0.27	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1299	1blx	B	69	224	1.1e-39			71.57	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1299	1blx	B	75	219	1.2e-31	0.44	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1299	1bu9	A	105	257	8.5e-39	0.01	0.84		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1299	1bu9	A	64	229	8.5e-39			67.86	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										P18INK4C, TUMOR, SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1299	1d9s	A	60	191	1.5e-34	0.29	1.00		CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT
1299	1ihb	A	105	256	5.1e-38	0.14	0.98		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1299	1ihb	A	138	263	3.4e-29	0.15	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1299	1ihb	A	69	223	5.1e-38			71.13	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1299	1ihb	A	70	221	4.4e-35	0.06	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6



Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1299	1ikn	D	133	262	3.4e-26	-0.14	0.15		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	INHIBITOR TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1299	1ikn	D	33	203	8.5e-39	0.02	0.82		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1299	1ikn	D	5	170	1.2e-34	0.04	0.72		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1299	1ikn	D	67	252	1.4e-45	-0.11	1.00		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1299	1ikn	D	68	263	6.6e-48			74.46	NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1299	1ikn	D	69	255	6.6e-48	-0.10	1.00		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1299	1myo		35	151	1.3e-30			56.75	MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLYATION, NMR, ANK-REPEAT
1299	1mfi	E	32	203	1e-39	0.30	1.00		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-	COMPLEX (TRANSCRIPTION REG/ANK REPEAT)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1299	1nfi	E	39	226	2e-45	0.50	1.00		KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1299	1nfi	E	5	170	1.2e-34	-0.11	0.74		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1299	1nfi	E	64	264	1.8e-46			75.28	NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1299	1nfi	E	65	255	1.8e-46	0.21	1.00		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1299	1nfi	E	66	252	3.4e-45	0.04	1.00		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1301	1bj8		361	452	6.6e-16	0.13	0.49		GP130; CHAIN: NULL;	RECEPTOR RECEPTOR, SIGNAL TRANSDUCER OF IL-6 TYPE CYTOKINES, THIRD 2 N-TERMINAL DOMAIN, TRANSMEMBRANE, GLYCOPROTEIN
1301	1bpv		357	457	1.8e-16	0.24	0.06		TITIN; CHAIN: NULL;	CONNECTIN A71, CONNECTIN; TITIN, CONNECTIN, FIBRONECTIN TYPE III
1301	1bqu	A	359	457	0.00044	0.14	0.12		GP130; CHAIN: A, B;	SIGNALING PROTEIN CYTOKINE RECEPTOR, GLYCOPROTEIN 130, GP130, INTERLEUKINE 6 2 RECEPTOR BETA SUBUNIT, SIGNALING PROTEIN
1301	1cto		353	452	4.4e-16	0.01	-0.13		GRANULOCYTE COLONY-STIMULATING FACTOR RECEPTOR; CHAIN: NULL;	BINDING PROTEIN BINDING PROTEIN, CYTOKINE RECEPTOR
1301	1fnf		356	481	1.3e-11	0.32	-0.14		FIBRONECTIN; 1FNF 6 CHAIN: NULL; 1FNF 7	CELL ADHESION PROTEIN RGD, EXTRACELLULAR MATRIX 1FNF 18
1301	1fnf		359	452	1.1e-13	0.38	0.42		FIBRONECTIN; 1FNF 6 CHAIN: NULL; 1FNF 7	CELL ADHESION PROTEIN RGD, EXTRACELLULAR MATRIX 1FNF 18
1301	1fnh	A	363	481	6.6e-11	0.11	0.16		FIBRONECTIN; CHAIN: A;	HEPARIN AND INTEGRIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										BINDING HEPARIN AND INTEGRIN BINDING
1301	1mfn		359	452	4.4e-13	0.64	0.27		FIBRONECTIN; CHAIN: NULL;	CELL ADHESION PROTEIN, CELL ADHESION PROTEIN, RGD, EXTRACELLULAR MATRIX, 2 HEPARIN-BINDING, GLYCOPROTEIN
1301	1mfn		362	524	4.4e-12	-0.01	0.55		FIBRONECTIN; CHAIN: NULL;	CELL ADHESION PROTEIN, CELL ADHESION PROTEIN, RGD, EXTRACELLULAR MATRIX, 2 HEPARIN-BINDING, GLYCOPROTEIN
1301	1qg3	A	362	452	2.2e-13	0.33	-0.05		INTEGRIN BETA-4 SUBUNIT; CHAIN: A, B;	STRUCTURAL PROTEIN INTEGRIN, HEMIDESMOSOME, FIBRONECTIN, CARCINOMA, STRUCTURAL 2 PROTEIN
1301	1tff		362	452	2.2e-15	0.13	0.13		GLYCOPROTEIN FIBRONECTIN (TENTH TYPE III MODULE) (NMR, 36 STRUCTURES) 1TTF 3	
1301	2fmb	A	356	448	1.5e-16	0.28	0.13		FIBRONECTIN; CHAIN: A;	PROTEIN BINDING ED-B, FIBRONECTIN, TYPEIII DOMAIN, ANGIOGENESIS, PROTEIN 2 BINDING
1306	1a79	A	103	169	5.1e-06	-0.36	0.98		TRNA ENDONUCLEASE; CHAIN: A, B, C, D;	ENDONUCLEASE ENDONUCLEASE, TRNA ENDONUCLEASE
1307	1f81	A	178	232	0.0012	-0.90	0.00		CREB-BINDING PROTEIN;	TRANSCRIPTION ZINC

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									CHAIN: A;	FINGER, TAZ2, CBP
1309	1av1	A	141	337	8.5e-09			63.71	APOLIPOPROTEIN A-I; CHAIN: A, B, C, D;	LIPID TRANSPORT APO A-I; LIPOPROTEIN, LIPID TRANSPORT, CHOLESTEROL METABOLISM, 2 ATHEROSCLEROSIS, HDL, LCAT-ACTIVATION
1309	1cun	A	115	321	6.6e-10			62.50	ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1309	1cun	A	90	324	6.6e-10	-0.20	0.13		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1311	1ffk	R	27	79	6.8e-18	0.01	0.36		23S RRNA; CHAIN: 0; 5S RRNA; CHAIN: 9; RIBOSOMAL PROTEIN L2; CHAIN: A; RIBOSOMAL PROTEIN L3; CHAIN: B; RIBOSOMAL PROTEIN L4; CHAIN: C; RIBOSOMAL PROTEIN L5; CHAIN: D;	RIBOSOME 50S RIBOSOMAL PROTEIN L2P, HMAL2, HL4; 50S RIBOSOMAL PROTEIN L3P, HMAL3, HL1; 50S RIBOSOMAL PROTEIN L4E, HMAL4, HL6; 50S RIBOSOMAL PROTEIN L5P,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									RIBOSOMAL PROTEIN L7AE; CHAIN: E; RIBOSOMAL PROTEIN L10E; CHAIN: F; RIBOSOMAL PROTEIN L13; CHAIN: G; RIBOSOMAL PROTEIN L14; CHAIN: H; RIBOSOMAL PROTEIN L15E; CHAIN: I; RIBOSOMAL PROTEIN L15; CHAIN: J; RIBOSOMAL PROTEIN L18; CHAIN: K; RIBOSOMAL PROTEIN L18E; CHAIN: L; RIBOSOMAL PROTEIN L19; CHAIN: M; RIBOSOMAL PROTEIN L21E; CHAIN: N; RIBOSOMAL PROTEIN L22; CHAIN: O; RIBOSOMAL PROTEIN L23; CHAIN: P; RIBOSOMAL PROTEIN L24; CHAIN: Q; RIBOSOMAL PROTEIN L24E; CHAIN: R; RIBOSOMAL PROTEIN L29; CHAIN: S; RIBOSOMAL PROTEIN L30; CHAIN: T; RIBOSOMAL PROTEIN L31E; CHAIN: U; RIBOSOMAL PROTEIN L32E; CHAIN: V; RIBOSOMAL PROTEIN L37AE; CHAIN: W; RIBOSOMAL PROTEIN L37E; CHAIN: X; RIBOSOMAL PROTEIN L39E; CHAIN: Y; RIBOSOMAL PROTEIN L44E;	HMAL5, HL13; 50S RIBOSOMAL PROTEIN HS6; 50S RIBOSOMAL PROTEIN L13P, HMAL13; 50S RIBOSOMAL PROTEIN L14P, HMAL14, HL27; 50S RIBOSOMAL PROTEIN L15P, HMAL15, HL9; 50S RIBOSOMAL PROTEIN L18P, HMAL18, HL12; 50S RIBOSOMAL PROTEIN L18E, HL29, L19; 50S RIBOSOMAL PROTEIN L19E, HMAL19, HL24; 50S RIBOSOMAL PROTEIN L21E, HL31; 50S RIBOSOMAL PROTEIN L22P, HMAL22, HL23; 50S RIBOSOMAL PROTEIN L23P, HMAL23, HL25, L21; 50S RIBOSOMAL PROTEIN L24P, HMAL24, HL16, HL15; 50S RIBOSOMAL PROTEIN L24E, HL21/HL22; 50S RIBOSOMAL PROTEIN L29P, HMAL29, HL33; 50S RIBOSOMAL PROTEIN L30P, HMAL30, HL20, HL16; 50S RIBOSOMAL PROTEIN L31E, L34, HL30; 50S RIBOSOMAL PROTEIN L32E, HL5; 50S RIBOSOMAL PROTEIN L37E, L35E; 50S

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									CHAIN: Z; RIBOSOMAL PROTEIN L6; CHAIN: 1;	RIBOSOMAL PROTEINS L39E, HL39E, HL46E; 50S RIBOSOMAL PROTEIN L44E, LA, HLA; 50S RIBOSOMAL PROTEIN L6P, HMAL6, HL10 RIBOSOME ASSEMBLY, RNA-RNA, PROTEIN-RNA, PROTEIN-PROTEIN
1311	1ffk	R	29	79	1.8e-24	-0.14	0.22		23S RRNA; CHAIN: 0; 5S RRNA; CHAIN: 9; RIBOSOMAL PROTEIN L2; CHAIN: A; RIBOSOMAL PROTEIN L3; CHAIN: B; RIBOSOMAL PROTEIN L4; CHAIN: C; RIBOSOMAL PROTEIN L5; CHAIN: D; RIBOSOMAL PROTEIN L7AF; CHAIN: E; RIBOSOMAL PROTEIN L10E; CHAIN: F; RIBOSOMAL PROTEIN L13; CHAIN: G; RIBOSOMAL PROTEIN L14; CHAIN: H; RIBOSOMAL PROTEIN L15E; CHAIN: I; RIBOSOMAL PROTEIN L15; CHAIN: J; RIBOSOMAL PROTEIN L18; CHAIN: K; RIBOSOMAL PROTEIN L18E; CHAIN: L; RIBOSOMAL PROTEIN L19; CHAIN: M; RIBOSOMAL PROTEIN L21E; CHAIN: N; RIBOSOMAL PROTEIN L22; CHAIN: O;	RIBOSOME 50S RIBOSOMAL PROTEIN L2P, HMAL2, HL4; 50S RIBOSOMAL PROTEIN L3P, HMAL3, HL1; 50S RIBOSOMAL PROTEIN L4E, HMAL4, HL6; 50S RIBOSOMAL PROTEIN L5P, HMAL5, HL13; 30S RIBOSOMAL PROTEIN HS6; 50S RIBOSOMAL PROTEIN L13P, HMAL13; 50S RIBOSOMAL PROTEIN L14P, HMAL14, HL27; 50S RIBOSOMAL PROTEIN L15P, HMAL15, HL9; 50S RIBOSOMAL PROTEIN L18P, HMAL18, HL12; 50S RIBOSOMAL PROTEIN L18E, HL29, L19; 50S RIBOSOMAL PROTEIN L19E, HMAL19, HL24; 50S RIBOSOMAL PROTEIN L21E, HL31; 50S RIBOSOMAL PROTEIN L22P,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									RIBOSOMAL PROTEIN L23; CHAIN: P; RIBOSOMAL PROTEIN L24; CHAIN: Q; RIBOSOMAL PROTEIN L24E; CHAIN: R; RIBOSOMAL PROTEIN L29; CHAIN: S; RIBOSOMAL PROTEIN L30; CHAIN: T; RIBOSOMAL PROTEIN L31E; CHAIN: U; RIBOSOMAL PROTEIN L32E; CHAIN: V; RIBOSOMAL PROTEIN L37AE; CHAIN: W; RIBOSOMAL PROTEIN L37E; CHAIN: X; RIBOSOMAL PROTEIN L39E; CHAIN: Y; RIBOSOMAL PROTEIN L44E; CHAIN: Z; RIBOSOMAL PROTEIN L6; CHAIN: 1;	HMAL22, HL23; 50S RIBOSOMAL PROTEIN L23P, HMAL23, HL25, L21; 50S RIBOSOMAL PROTEIN L24P, HMAL24, HL16, HL15; 50S RIBOSOMAL PROTEIN L24E, HL21/HL22; 50S RIBOSOMAL PROTEIN L29P, HMAL29, HL33; 50S RIBOSOMAL PROTEIN L30P, HMAL30, HL20, HL16; 50S RIBOSOMAL PROTEIN L31E, L34, HL30; 50S RIBOSOMAL PROTEIN L32E, HL5; 50S RIBOSOMAL PROTEIN L37E, L35E; 50S RIBOSOMAL PROTEINS L39E, HL39E, HL46E; 50S RIBOSOMAL PROTEIN L44E, LA, HLA; 50S RIBOSOMAL PROTEIN L6P, HMAL6, HL10 RIBOSOME ASSEMBLY, RNA-RNA, PROTEIN-RNA, PROTEIN-PROTEIN
1314	1crz	A	708	805	0.0019	0.08	0.11		TOLB PROTEIN; CHAIN: A;	TOXIN BINDING PROTEIN TWO DOMAINS: BETA PROPELLER AND ALPHA/BETA FOLD
1314	1erj	A	429	695	1.7e-41	0.16	-0.12		TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	TRANSCRIPTION INHIBITOR BETA-PROPELLER
1314	1erj	A	449	782	1.7e-63	0.42	0.93		TRANSCRIPTIONAL REPRESSOR	TRANSCRIPTION INHIBITOR



Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1314	1ejj	A	543	805	1.7e-48	0.46	1.00		TUPI; CHAIN: A, B, C; TRANSCRIPTIONAL REPRESSOR TUPI; CHAIN: A, B, C;	BETA-PROPELLER TRANSCRIPTION INHIBITOR BETA-PROPELLER
1314	1got	B	403	779	1.4e-71			95.77	GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP- BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP- BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
1314	1got	B	430	779	1.4e-71	0.41	1.00		GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP- BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP- BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
1314	1got	B	534	804	3.4e-48	0.37	1.00		GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP- BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP- BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1318	1d0s	A	2	170	1.1e-08	0.44	-0.20		NICOTINATE MONONUCLEOTIDE:5,6- CHAIN: A;	TRANSFERASE DINUCLEOTIDE-BINDING MOTIF, PHOSPHORIBOSYL TRANSFERASE
1318	1d0s	A	20	365	1.3e-20	0.63	-0.19		NICOTINATE MONONUCLEOTIDE:5,6- CHAIN: A;	TRANSFERASE DINUCLEOTIDE-BINDING MOTIF, PHOSPHORIBOSYL TRANSFERASE
1318	1d0s	A	228	590	1.8e-09	0.23	-0.19		NICOTINATE MONONUCLEOTIDE:5,6- CHAIN: A;	TRANSFERASE DINUCLEOTIDE-BINDING MOTIF, PHOSPHORIBOSYL TRANSFERASE
1318	1d0s	A	378	740	6.6e-10	0.01	-0.20		NICOTINATE MONONUCLEOTIDE:5,6- CHAIN: A;	TRANSFERASE DINUCLEOTIDE-BINDING MOTIF, PHOSPHORIBOSYL TRANSFERASE
1318	1d0s	A	5	136	1.8e-09	0.36	-0.20		NICOTINATE MONONUCLEOTIDE:5,6- CHAIN: A;	TRANSFERASE DINUCLEOTIDE-BINDING MOTIF, PHOSPHORIBOSYL TRANSFERASE
1318	1osm	A	6	238	4.4e-16	0.90	-0.20		OMP36; CHAIN: A, B, C;	OUTER MEMBRANE PROTEIN OSMOPORIN; OUTER MEMBRANE PROTEIN, NON-SPECIFIC PORIN, OSMOPORIN, 2 BETA-BARREL, TRANSMEMBRANE
1318	1qq4	A	13	157	4.4e-09	1.12	-0.14		ALPHA-LYTIC PROTEASE; CHAIN: A;	HYDROLASE DOUBLE BETA BARREL, BACTERIAL SERINE PROTEASE
1318	1tal		2	156	2.2e-09	1.15	-0.19		ALPHA-LYTIC PROTEASE;	SERINE PROTEASE SERINE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									CHAIN: NULL;	PROTEASE, LOW TEMPERATURE, HYDROLASE, 2 SERINE PROTEINASE
1318	2omf		13	235	8.8e-16	1.01	-0.20		MATRIX PORIN OUTER MEMBRANE PROTEIN F; 2OMF 5 CHAIN: NULL; 2OMF 6	INTEGRAL MEMBRANE PROTEIN PORIN MATRIX PORIN, OMPF PORIN; 2OMF 7 PORIN, MEMBRANE PROTEIN 2OMF 12
1318	2omf		26	363	1.3e-15	0.81	-0.19		MATRIX PORIN OUTER MEMBRANE PROTEIN F; 2OMF 5 CHAIN: NULL; 2OMF 6	INTEGRAL MEMBRANE PROTEIN PORIN MATRIX PORIN, OMPF PORIN; 2OMF 7 PORIN, MEMBRANE PROTEIN 2OMF 12
1318	4ubp	C	413	744	4.4e-09	0.02	-0.17		UREASE (CHAIN A); CHAIN: A; UREASE (CHAIN B); CHAIN: B; UREASE (CHAIN C); CHAIN: C;	HYDROLASE UREA AMINOHYDROLASE; UREA AMINOHYDROLASE; UREA AMINOHYDROLASE; UREASE, BACILLUS PASTEURII, NICKEL, ACETOHYDROXAMIC ACID, 2 METALLOENZYME
1324	1fjg	J	19	97	1.4e-26	0.32	0.60		16S RIBOSOMAL RNA; CHAIN: A; FRAGMENT OF MESSENGER RNA; CHAIN: X; 30S RIBOSOMAL PROTEIN S2; CHAIN: B; 30S RIBOSOMAL PROTEIN S3; CHAIN: C; 30S RIBOSOMAL PROTEIN S4; CHAIN: D; 30S RIBOSOMAL	RIBOSOME 30S RIBOSOMAL SUBUNIT, RIBOSOME, ANTIBIOTIC, STREPTOMYCIN, 2 SPECTINOMYCIN, PAROMOMYCIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									PROTEIN S5; CHAIN: E; 30S RIBOSOMAL PROTEIN S6; CHAIN: F; 30S RIBOSOMAL PROTEIN S7; CHAIN: G; 30S RIBOSOMAL PROTEIN S8; CHAIN: H; 30S RIBOSOMAL PROTEIN S9; CHAIN: I; 30S RIBOSOMAL PROTEIN S10; CHAIN: J; 30S RIBOSOMAL PROTEIN S11; CHAIN: K; 30S RIBOSOMAL PROTEIN S12; CHAIN: L; 30S RIBOSOMAL PROTEIN S13; CHAIN: M; 30S RIBOSOMAL PROTEIN S14; CHAIN: N; 30S RIBOSOMAL PROTEIN S15; CHAIN: O; 30S RIBOSOMAL PROTEIN S16; CHAIN: P; 30S RIBOSOMAL PROTEIN S17; CHAIN: Q; 30S RIBOSOMAL PROTEIN S18; CHAIN: R; 30S RIBOSOMAL PROTEIN S19; CHAIN: S; 30S RIBOSOMAL PROTEIN S20; CHAIN: T; 30S RIBOSOMAL PROTEIN THX; CHAIN: V	
1325	1a1h	A	719	741	0.008	-0.14	0.95		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1325	1ahd	P	1015	1075	1.7e-31	0.43	0.42		DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 1AHD 3 REPLACED BY SER (C39S) COMPLEX WITH DNA (NMR, 1AHD 4 16 STRUCTURES) 1AHD 5	
1325	1ahd	P	545	605	5.1e-32	0.17	0.78		DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 1AHD 3 REPLACED BY SER (C39S) COMPLEX WITH DNA (NMR, 1AHD 4 16 STRUCTURES) 1AHD 5	
1325	1ahd	P	807	873	1.2e-32	0.19	0.84		DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 1AHD 3 REPLACED BY SER (C39S) COMPLEX WITH DNA (NMR, 1AHD 4 16 STRUCTURES) 1AHD 5	
1325	1b72	A	1019	1076	5.1e-26	0.51	0.43		HOMEODOMAIN PROTEIN HOX-B1; CHAIN: A; PBX1; CHAIN: B; DNA CHAIN: D; DNA CHAIN: E;	PROTEIN/DNA HOMEODOMAIN, DNA, COMPLEX, DNA-BINDING PROTEIN, PROTEIN/DNA
1325	1b72	A	549	606	1e-26	0.21	1.00		HOMEODOMAIN PROTEIN HOX-B1; CHAIN: A; PBX1; CHAIN: B; DNA CHAIN: D; DNA CHAIN: E;	PROTEIN/DNA HOMEODOMAIN, DNA, COMPLEX, DNA-BINDING PROTEIN, PROTEIN/DNA
1325	1b72	A	811	868	1.7e-26	0.51	0.92		HOMEODOMAIN PROTEIN HOX-B1; CHAIN: A; PBX1; CHAIN: B; DNA	PROTEIN/DNA HOMEODOMAIN, DNA,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1325	1b8i	A	1019	1073	1e-26	0.39	0.71		CHAIN: D; DNA CHAIN: E;	COMPLEX, DNA-BINDING PROTEIN, PROTEIN/DNA TRANSCRIPTION/DNA
1325	1b8i	A	549	603	1e-27	0.37	1.00		ULTRABITHORAX HOMEOTIC PROTEIN IV; CHAIN: A; HOMEODOMAIN, HOMEOBOX PROTEIN EXTRADENTICLE; CHAIN: B; DNA (5'-CHAIN: C; DNA (5'-CHAIN: D;	ULTRABITHORAX; PBX PROTEIN; DNA BINDING, HOMEODOMAIN, HOMEOTIC PROTEINS, DEVELOPMENT, 2 SPECIFICITY
1325	1b8i	A	811	865	8.5e-27	0.54	0.75		ULTRABITHORAX HOMEOTIC PROTEIN IV; CHAIN: A; HOMEODOMAIN, HOMEOBOX PROTEIN EXTRADENTICLE; CHAIN: B; DNA (5'-CHAIN: C; DNA (5'-CHAIN: D;	TRANSCRIPTION/DNA ULTRABITHORAX; PBX PROTEIN; DNA BINDING, HOMEODOMAIN, HOMEOTIC PROTEINS, DEVELOPMENT, 2 SPECIFICITY
1325	1bw5		1013	1076	4e-19	-0.11	0.34		INSULIN GENE ENHANCER PROTEIN ISL-1; CHAIN: NULL;	DNA-BINDING PROTEIN ISL-1HD DNA-BINDING PROTEIN, HOMEODOMAIN, LIM DOMAIN
1325	1enh		547	599	1.7e-18	0.13	0.98		DNA-BINDING PROTEIN ENGRAILED HOMEODOMAIN 1ENH 3	
1325	1enh		809	861	5.1e-18	0.64	1.00		DNA-BINDING PROTEIN	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									ENGRAILED HOMEODOMAIN IENH 3	
1325	1fj1	A	1015	1074	1.7e-24	0.50	0.99		PAIRED PROTEIN; CHAIN: A, B, C; DNA; CHAIN: D, E, F	COMPLEX (DNA-BINDING PROTEIN/DNA) DNA-BINDING PROTEIN, DNA, PAIRED BOX, TRANSCRIPTION 2 REGULATION
1325	1fj1	A	544	604	8.5e-24	0.15	1.00		PAIRED PROTEIN; CHAIN: A, B, C; DNA; CHAIN: D, E, F	COMPLEX (DNA-BINDING PROTEIN/DNA) DNA-BINDING PROTEIN, DNA, PAIRED BOX, TRANSCRIPTION 2 REGULATION
1325	1fj1	A	806	866	1.5e-23	0.41	1.00		PAIRED PROTEIN; CHAIN: A, B, C; DNA; CHAIN: D, E, F	COMPLEX (DNA-BINDING PROTEIN/DNA) DNA-BINDING PROTEIN, DNA, PAIRED BOX, TRANSCRIPTION 2 REGULATION
1325	1fj1	B	1015	1072	8.5e-24	0.43	0.87		PAIRED PROTEIN; CHAIN: A, B, C; DNA; CHAIN: D, E, F	COMPLEX (DNA-BINDING PROTEIN/DNA) DNA-BINDING PROTEIN, DNA, PAIRED BOX, TRANSCRIPTION 2 REGULATION
1325	1fj1	B	545	602	1e-22	0.19	0.98		PAIRED PROTEIN; CHAIN: A, B, C; DNA; CHAIN: D, E, F	COMPLEX (DNA-BINDING PROTEIN/DNA) DNA-BINDING PROTEIN, DNA, PAIRED BOX, TRANSCRIPTION 2

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1325	1fj1	B	807	864	1.7e-22	0.40	1.00		PAIRED PROTEIN; CHAIN: A, B, C; DNA; CHAIN: D, E, F	REGULATION COMPLEX (DNA-BINDING PROTEIN/DNA) DNA-BINDING PROTEIN, DNA, PAIRED BOX, TRANSCRIPTION 2 REGULATION
1325	1ftz		1016	1073	5.1e-27	0.56	0.46		DNA-BINDING FUSHI TARAZU PROTEIN (HOMEODOMAIN) (NMR, 20 STRUCTURES) IFTZ 3	
1325	1ftz		546	603	8.5e-27	0.37	0.66		DNA-BINDING FUSHI TARAZU PROTEIN (HOMEODOMAIN) (NMR, 20 STRUCTURES) IFTZ 3	
1325	1ftz		808	872	5.1e-27	0.27	0.57		DNA-BINDING FUSHI TARAZU PROTEIN (HOMEODOMAIN) (NMR, 20 STRUCTURES) IFTZ 3	
1325	1mey	C	140	223	3.4e-05	-0.57	0.07		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1325	1san		1021	1075	1.4e-28	0.91	0.65		DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 1SAN 3 REPLACED BY SER AND RESIDUES 1-6 DELETED (C39S, DEL 1-6) 1SAN 4 (NMR, 20 STRUCTURES) 1SAN 5	
1325	1san		551	605	1.7e-29	0.33	0.99		DNA-BINDING PROTEIN	



Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 1SAN 3 REPLACED BY SER AND RESIDUES 1-6 DELETED (C39S,DEL 1-6) 1SAN 4 (NMR, 20 STRUCTURES) 1SAN 5	
1325	1san		813	873	6.8e-30	0.67	0.87		DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 1SAN 3 REPLACED BY SER AND RESIDUES 1-6 DELETED (C39S,DEL 1-6) 1SAN 4 (NMR, 20 STRUCTURES) 1SAN 5	
1325	1ubd	C	139	218	2e-07	-0.20	0.12		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1325	2adr		139	218	1e-08	-0.09	0.03		ADR1; CHAIN: NULL;	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ADR1, ZINC FINGER, NMR
1325	2dirp	A	196	222	4e-05	-0.16	0.04		COMPLEX(TRANSCRIPTION REGULATION/DNA) TRAMTRACK PROTEIN (TWO ZINC-FINGER PEPTIDE)	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									COMPLEXED WITH 2DRP 3 DNA 2DRP 4	
1325	2gli	A	139	218	2e-07	0.14	0.30		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1325	2hdd	B	1016	1071	5.1e-19	0.59	0.99		ENGRAILED HOMEODOMAIN; CHAIN: A, B; DNA (20-MER); CHAIN: C, D;	COMPLEX (DNA BINDING PROTEIN/DNA) DNA BINDING, COMPLEX (DNA BINDING PROTEIN/DNA)
1325	2hdd	B	546	601	1.4e-18	0.36	0.96		ENGRAILED HOMEODOMAIN; CHAIN: A, B; DNA (20-MER); CHAIN: C, D;	COMPLEX (DNA BINDING PROTEIN/DNA) DNA BINDING, COMPLEX (DNA BINDING PROTEIN/DNA)
1325	2hdd	B	808	863	3.4e-18	0.56	0.98		ENGRAILED HOMEODOMAIN; CHAIN: A, B; DNA (20-MER); CHAIN: C, D;	COMPLEX (DNA BINDING PROTEIN/DNA) DNA BINDING, COMPLEX (DNA BINDING PROTEIN/DNA)
1325	3znf		1445	1472	0.008	-0.30	0.27		ZINC FINGER /DNA\$ BINDING DOMAIN ZINC FINGER (NMR\$) 3ZNF 3	
1325	9ant	A	1019	1074	5.1e-29	0.47	0.74		ANTENNAPEDIA PROTEIN; CHAIN: A, B; DNA; CHAIN: C, D, E, F;	COMPLEX (DNA-BINDING PROTEIN/DNA) HD; HOMEODOMAIN, COMPLEX (DNA-BINDING PROTEIN/DNA)
1325	9ant	A	549	604	6.8e-30	0.36	1.00		ANTENNAPEDIA PROTEIN; CHAIN: A, B; DNA; CHAIN: C, D, E, F;	COMPLEX (DNA-BINDING PROTEIN/DNA) HD; HOMEODOMAIN, COMPLEX (DNA-BINDING

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1325	9ant	A	811	866	1.7e-29	0.46	1.00		ANTENNAPEDIA PROTEIN; CHAIN: A, B; DNA; CHAIN: C, D, E, F;	PROTEIN/DNA) COMPLEX (DNA-BINDING PROTEIN/DNA) HD; HOMEODOMAIN, COMPLEX (DNA-BINDING PROTEIN/DNA)
1327	1a5e		5	117	6.8e-18	0.51	1.00		TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT
1327	1a5e		6	114	6e-18	-0.12	0.15		TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT
1327	1awc	B	1	152	1.2e-41			55.04	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1327	1awc	B	36	186	6.8e-38	0.02	0.60		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1327	1awc	B	5	150	1.2e-41	0.30	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1327	1b0x	A	350	408	0.0012	0.01	0.19		EPHA4 RECEPTOR TYROSINE KINASE; CHAIN: A;	TRANSFERASE RECEPTOR TYROSINE KINASE, PROTEIN INTERACTION MODULE, 2 DIMERIZATION DOMAIN, TRANSFERASE
1327	1b4f	A	346	408	0.0037	0.38	0.41		EPHB2; CHAIN: A, B, C, D, E, F, G, H;	SIGNAL TRANSDUCTION SAM DOMAIN, EPH RECEPTOR, SIGNAL TRANSDUCTION, OLIGOMER
1327	1b4f	A	351	408	2.4e-06	0.33	0.43		EPHB2; CHAIN: A, B, C, D, E, F, G, H;	SIGNAL TRANSDUCTION SAM DOMAIN, EPH RECEPTOR, SIGNAL TRANSDUCTION, OLIGOMER
1327	1bd8		1	154	3.4e-35			51.63	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1327	1bd8		39	189	3.4e-35	0.09	-0.08		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1327	1bi7	B	5	117	8.5e-19	0.38	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; MULTIPLE TUMOR SUPPRESSOR; CHAIN: B;	ANKYRIN MOTIF COMPLEX (KINASE/ANTI-ONCOGENE) CDK6; P16INK4A, MTS1; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, MULTIPLE TUMOR SUPPRESSOR, 3 MTS1, COMPLEX (KINASE/ANTI-ONCOGENE) HEADER
1327	1blx	B	1	157	1e-34			53.01	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1327	1blx	B	39	189	1e-34	0.32	0.05		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1327	1bu9	A	1	163	6.8e-39			54.97	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										P18INK4C, TUMOR, SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1327	1bu9	A	2	56	3.4e-07	0.03	0.87		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1327	1bu9	A	36	191	6.8e-39	0.12	-0.08		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1327	1bu9	A	5	158	1.7e-34	0.43	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1327	1d9s	A	3	117	3.6e-25	0.61	1.00		CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	SIGNALING PROTEIN HELIX-TURN-HELIX,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1327	1d9s	A	5	123	1.7e-19	0.33	1.00		CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	ANKYRIN REPEAT SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT
1327	1dcq	A	5	117	5.1e-17	0.38	1.00		PYK2-ASSOCIATED PROTEIN BETA; CHAIN: A;	METAL BINDING PROTEIN ZINC-BINDING MODULE, ANKYRIN REPEATS, METAL BINDING PROTEIN
1327	1hhb	A	1	155	3.4e-38			56.55	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18- INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1327	1hhb	A	36	190	3.4e-38	0.02	0.13		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18- INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1327	1hhb	A	5	154	1.2e-33	0.16	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18- INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1327	1ikn	D	5	186	1.7e-38	0.02	0.84		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B- ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1327	1myo		1	114	1.1e-27	0.27	0.99		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT
1327	1myo		33	148	1.1e-27			54.26	MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT
1327	1myo		6	119	1.7e-24	0.35	1.00		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT
1327	1nfi	E	5	186	3.4e-38	0.02	0.98		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1327	1sgg		352	399	0.0012	-0.31	0.31		EPHRIN TYPE-B RECEPTOR 2; CHAIN: NULL;	TYROSINE-PROTEIN KINASE NMR, RECEPTOR OLIGOMERIZATION, EPH RECEPTORS, TYROSINE 2 PHOSPHORYLATION, SIGNAL TRANSDUCTION, TYROSINE-PROTEIN 3 KINASE
1327	1ycs	B	35	235	1.2e-22			53.24	P53; CHAIN: A; 53BP2; CHAIN: B;	COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS) P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR



Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI- ONCOGENE/ANKYRIN REPEATS)
1327	1ycs	B	5	93	1.7e-20	0.20	1.00		P53; CHAIN: A; 53BP2; CHAIN: B;	COMPLEX (ANTI- ONCOGENE/ANKYRIN REPEATS) P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI- ONCOGENE/ANKYRIN REPEATS)
1330	1alh	A	233	313	3.4e-27	-0.16	0.58		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1330	1mey	C	201	285	5.1e-42	0.02	0.06		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1330	1mey	C	232	313	1e-45	-0.06	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1330	1mey	C	260	341	1.5e-46	0.09	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1330	1mey	C	288	369	6.8e-48	0.14	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1330	1mey	C	316	397	3.4e-48	-0.11	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1330	1mey	C	344	425	1.4e-49	-0.31	1.00		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1330	1mey	C	372	453	1e-49	0.32	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1330	1mey	C	400	481	1.2e-50	0.60	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1330	1mey	C	400	482	5.1e-51			100.78	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1330	1mey	C	428	509	5.1e-51	0.52	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1330	1mey	C	456	537	1.5e-50	0.64	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1330	1mey	C	512	593	1.7e-50	0.19	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1330	1mey	C	540	621	5.1e-50	0.25	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1330	1mey	C	540	650	2.4e-37	0.04	0.83		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1330	1mey	C	568	649	5.1e-50	0.18	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1330	1mey	C	596	657	1.7e-37	0.13	0.30		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1330	1tf6	A	202	350	1.7e-32	-0.25	0.53		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1330	1tf6	A	228	369	3.6e-52	-0.08	0.92		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1330	1tf6	A	239	397	3.6e-55	-0.50	0.37		TFIIIA; CHAIN: A, D; 5S	COMPLEX (TRANSCRIPTION

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1330	1ff6	A	261	406	1.7e-36	-0.57	0.90		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1330	1ff6	A	289	481	2.4e-71	-0.11	0.54		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1330	1ff6	A	373	518	1.7e-37	0.16	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1330	1ff6	A	373	537	1.2e-76	0.04	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1330	1ff6	A	400	563	3.6e-77			100.48	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1330	1ff6	A	429	593	3.6e-77	0.17	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1330	1ff6	A	457	639	2.4e-67	0.10	0.95		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1330	1tf6	A	485	631	3.4e-37	0.04	0.99		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	PROTEIN COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1330	1tf6	A	513	657	1e-37	-0.00	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1330	1tf6	A	513	657	4.8e-47	0.08	0.87		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1330	1ubd	C	153	257	3.4e-25	0.15	-0.19		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-



Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1330	1ubd	C	209	313	1.5e-29	-0.09	0.28		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1330	1ubd	C	235	341	3.4e-32	-0.06	0.70		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1330	1ubd	C	260	369	1.1e-53	-0.27	0.94		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1330	1ubd	C	314	453	7.2e-51	-0.25	0.74		YY1; CHAIN: C; ADENO-	COMPLEX (TRANSCRIPTION REGULATION/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1330	1ubd	C	324	425	1.7e-33	-0.31	0.74		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1330	1ubd	C	352	453	8.5e-35	-0.02	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1330	1ubd	C	398	509	9.6e-59	0.20	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1330	1ubd	C	402	510	9.6e-59			80.93	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1330	1ubd	C	408	509	1e-35	0.21	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1330	1ubd	C	454	565	1.1e-57	0.21	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1330	1ubd	C	510	646	2.4e-46	-0.04	0.86		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1330	1ubd	C	548	649	1e-34	0.19	0.64		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1330	2gli	A	201	340	3.4e-32	-0.24	0.66		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1330	2gli	A	234	370	2.4e-56	0.12	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1330	2gli	A	260	399	1.2e-65	-0.10	0.84		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1330	2gli	A	344	483	1.2e-71			89.49	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1330	2gli	A	344	483	1.2e-71	0.28	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1330	2gli	A	428	567	8.4e-76	0.44	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1330	2gli	A	484	646	3.6e-63	-0.06	0.95		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1330	2gli	A	520	651	5.1e-34	0.20	0.77		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1332	1e01	A	70	96	0.0011	0.07	0.36		FORMIN BINDING PROTEIN; CHAIN: A;	SH3 DOMAIN WW DOMAIN, FBP28, SIGNAL TRANSDUCTION

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1332	1e0m	A	70	95	0.0044	0.11	0.52		WWPROTOTYPE; CHAIN: A;	SH3 PROTOTYPE WWPROTOTYPE, PROTEIN DESIGN
1332	1pbw	A	909	1079	1.7e-18	0.42	0.96		PHOSPHATIDYLINOSITOL 3-KINASE; CHAIN: A, B;	PHOSPHOTRANSFERASE RHOGAP DOMAIN; PHOSPHOTRANSFERASE, TPASE ACTIVATING PROTEIN, GAP, CDC42, 2 PHOSPHOINOSITIDE 3-KINASE, SH3 DOMAIN, SH2 DOMAIN, 3 SIGNAL TRANSDUCTION
1332	1pbw	A	912	1081	4.4e-30	0.47	0.89		PHOSPHATIDYLINOSITOL 3-KINASE; CHAIN: A, B;	PHOSPHOTRANSFERASE RHOGAP DOMAIN; PHOSPHOTRANSFERASE, TPASE ACTIVATING PROTEIN, GAP, CDC42, 2 PHOSPHOINOSITIDE 3-KINASE, SH3 DOMAIN, SH2 DOMAIN, 3 SIGNAL TRANSDUCTION
1332	1pbw	B	907	1088	2.2e-31	0.23	0.74		PHOSPHATIDYLINOSITOL 3-KINASE; CHAIN: A, B;	PHOSPHOTRANSFERASE RHOGAP DOMAIN; PHOSPHOTRANSFERASE, TPASE ACTIVATING PROTEIN, GAP, CDC42, 2 PHOSPHOINOSITIDE 3-KINASE, SH3 DOMAIN, SH2 DOMAIN, 3 SIGNAL TRANSDUCTION
1332	1pbw	B	909	1079	1.7e-18	0.05	1.00		PHOSPHATIDYLINOSITOL 3-	PHOSPHOTRANSFERASE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									KINASE; CHAIN: A, B;	RHOGAP DOMAIN; PHOSPHOTRANSFERASE, TPASE ACTIVATING PROTEIN, GAP, CDC42, 2 PHOSPHOINOSITIDE 3-KINASE, SH3 DOMAIN, SH2 DOMAIN, 3 SIGNAL TRANSDUCTION
1332	1rgp		888	1086	3.4e-43	0.33	1.00		RHOGAP; CHAIN: NULL;	G-PROTEIN CDC42 GTPASE-ACTIVATING PROTEIN; G-PROTEIN, GAP, SIGNAL-TRANSDUCTION
1332	1tx4	A	891	1086	3.4e-44	0.35	1.00		P50-RHOGAP; CHAIN: A; TRANSFORMING PROTEIN RHOA; CHAIN: B;	COMPLEX(GTPASE ACTIVATN/PROTO-ONCOGENE) GTPASE-ACTIVATING PROTEIN RHOGAP; COMPLEX (GTPASE ACTIVATION/PROTO-ONCOGENE), GTPASE, 2 TRANSITION STATE, GAP
1333	1a9n	A	46	148	1.4e-07	0.22	0.41		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1333	1a9n	A	48	129	1.7e-08	0.10	0.42		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA),

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										RNA, SNRNP, RIBONUCLEOPROTEIN
1333	1a9n	C	46	148	1.4e-07	0.05	0.46		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1333	1a9n	C	48	129	1.7e-08	0.16	0.34		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1333	1d0b	A	42	188	5.1e-17	0.35	1.00		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1333	1d0b	A	66	217	1.7e-08	0.14	0.52		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1333	1d0b	A	7	144	1.5e-19	0.63	1.00		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1333	1dce	A	35	127	5.1e-11	0.31	0.69		RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 Å 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA



Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1333	1dce	A	46	172	5.1e-13	0.24	0.22		RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B, D;	SUBUNIT TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1333	1ds9	A	36	149	6.8e-14	0.00	0.64		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1333	1fo1	B	41	103	8.5e-08	-0.17	0.07		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
1334	4tmk	A	1025	1053	0.0084	-0.42	0.03		THYMIDYLATE KINASE; CHAIN: A;	TRANSFERASE ATP:DTMP PHOSPHOTRANSFERASE
1337	1bq0		9	89	1.7e-30	0.35	0.64		DNAJ; CHAIN: NULL;	CHAPERONE HSP40; CHAPERONE, HEAT SHOCK, PROTEIN FOLDING, DNAK
1337	1faf	A	23	80	2e-06	0.14	0.11		LARGE T ANTIGEN; CHAIN: A;	VIRUS/VIRAL PROTEIN J DOMAIN, HPD MOTIF, ANTI-PARALLEL HAIRPIN OF

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1337	1hdj		10	88	1e-29	0.62	1.00		HUMAN HSP40; CHAIN: NULL;	HELICES MOLECULAR CHAPERONE HDJ-1; MOLECULAR CHAPERONE
1339	1d2h	A	55	171	1.7e-15	0.18	-0.06		GLYCINE N-METHYLTRANSFERASE; CHAIN: A, B, C, D;	TRANSFERASE METHYLTRANSFERASE
1339	1d2h	A	61	210	4.4e-12	0.35	0.72		GLYCINE N-METHYLTRANSFERASE; CHAIN: A, B, C, D;	TRANSFERASE METHYLTRANSFERASE
1339	1xva	A	6	171	1.7e-19	-0.19	0.42		GLYCINE N-METHYLTRANSFERASE; CHAIN: A, B;	METHYLTRANSFERASE GNMT, S-ADENOSYL-L-METHIONINE; GLYCINE METHYLTRANSFERASE
1339	2adm	A	58	186	1.7e-09	0.14	0.47		ADENINE-N6-DNA-METHYLTRANSFERASE TAQI; CHAIN: A, B;	METHYLTRANSFERASE TRANSFERASE, METHYLTRANSFERASE, RESTRICTION SYSTEM
1349	1a1h	A	196	273	3.4e-27	-0.11	0.05		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1349	1a1h	A	228	301	6.8e-28	0.51	0.62		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1349	1a1h	A	333	415	2.4e-43			80.29	QGSR ZINC FINGER PEPTIDE;	COMPLEX (ZINC

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1349	1alh	A	361	441	2.4e-43	0.09	1.00		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1349	1alh	A	361	441	8.5e-32	0.01	1.00		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1349	1alh	A	389	445	9.6e-28	0.24	0.99		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1349	1alh	A	389	446	1.7e-22	0.54	0.99		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1349	1b8t	A	245	439	6e-17			60.74	CRP1; CHAIN: A;	CONTRACTILE LIM DOMAIN, CRP, NMR, MUSCLE DIFFERENTIATION, CONTRACTILE
1349	1mey	C	223	301	3.4e-46	0.18	0.98		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1349	1mey	C	248	329	1e-50	0.49	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1349	1mey	C	276	357	1.4e-50	0.44	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1349	1mey	C	276	358	3.4e-51			104.85	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1349	1mey	C	304	385	3.4e-51	0.27	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1349	1mey	C	360	441	6.8e-51	0.32	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	(ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1349	1mey	C	388	446	1.7e-35	0.46	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1349	1mey	G	58	86	1.7e-08	0.19	-0.19		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1349	1tf3	A	199	304	1.1e-13	-0.09	0.05		TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1349	1tf3	A	246	332	1.1e-13			60.20	TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E, F;	REGULATION/DNA
1349	1tf6	A	226	385	2.4e-60	0.07	0.89		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1349	1tf6	A	228	366	1e-35	0.18	0.87		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1349	1tf6	A	247	418	1.2e-75			110.06	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1349	1ff6	A	249	401	1.7e-37	0.28	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1349	1ff6	A	251	413	6e-72	0.03	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1349	1ff6	A	277	423	5.1e-38	-0.08	0.99		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1349	1ff6	A	277	441	1.2e-75	0.02	0.98		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1349	1tf6	A	305	443	5.1e-37	0.24	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1349	1ubd	C	198	301	1.2e-22	0.06	0.77		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1349	1ubd	C	225	329	1.7e-34	0.23	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)



Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1349	1ubd	C	228	329	2.4e-42	0.33	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1349	1ubd	C	248	358	1.1e-55			93.07	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1349	1ubd	C	251	357	1.1e-55	0.41	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1349	1ubd	C	284	385	6.8e-35	0.10	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1349	1ubd	C	302	413	1.2e-55	0.17	1.00		YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1349	1ubd	C	330	442	2.4e-55	0.12	1.00		YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1349	1ubd	C	340	441	1.7e-35	0.03	1.00		YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1349	2gli	A	198	331	2.4e-43	0.14	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	REGULATION/DNA)
1349	2gli	A	228	356	3.4e-34	0.25	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1349	2gli	A	240	359	4.8e-57	0.55	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1349	2gli	A	248	387	1.1e-71			103.49	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1349	2gli	A	276	415	1.1e-71	0.29	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1349	2gli	A	304	445	3.6e-56	0.10	0.99		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1349	2gli	A	312	443	3.4e-34	0.29	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1350	1bdq	A	149	246	0.0096	-0.18	0.11		HIV-1 PROTEASE; CHAIN: A, B;	HYDROLASE HYDROLASE, AIDS, POLYPROTEIN, ASPARTYL PROTEASE, ACID 2 PROTEASE, HYDROXYETHYLENE ISOSTERE INHIBITOR, SUBSTRATE 3 ANALOGUE INHIBITOR
1350	1daz	C	149	246	0.00084	0.17	0.37		PEPTIDE INHIBITOR; CHAIN: A, B; HIV-1 PROTEASE (RETROPEPSIN); CHAIN: C, D;	HYDROLASE HIV-1 PROTEASE, MUTANT, DIMER, INHIBITOR, OCCUPANCY
1351	1aww		280	340	1e-16	0.57	0.82		BRUTON'S TYROSINE KINASE; CHAIN: NULL;	TRANSFERASE ATK, AMGX1, BPK; TYROSINE KINASE, X-LINKED AGAMMAGLOBULINEMIA, XLA, BTK, SH3 2 DOMAIN, TRANSFERASE
1351	1bu1	A	289	341	5.1e-16	0.33	0.93		HEMOPOIETIC CELL KINASE; CHAIN: A, B, C, D, E, F;	TRANSFERASE TYROSINE-PROTEIN KINASE, TRANSFERASE, SIGNAL TRANSDUCTION, 2 SH3
1351	1efn	A	289	341	1e-18	0.43	0.87		FYN TYROSINE KINASE; CHAIN: A, C; HIV-1 NEF PROTEIN;	COMPLEX (SH3 DOMAIN/VIRAL

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									CHAIN: B, D;	ENHANCER SRC-HOMOLOGY 3 DOMAIN; COMPLEX (SH3 DOMAIN/VIRAL ENHANCER), PROTO-ONCOGENE, 2 TRANSFERASE, TYROSINE-PROTEIN KINASE, PHOSPHORYLATION, 3 AIDS, MYRISTYLATION, GTP-BINDING, ATP-BINDING, SH3 DOMAIN, 4 SH2 DOMAIN, PPII HELIX, PXXP MOTIF
1351	1faq		103	152	1.7e-14	-0.33	0.06		RAF-1; CHAIN: NULL;	SERINE/THREONINE PROTEIN KINASE TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, 2 PROTO-ONCOGENE, ZINC, ATP-BINDING, PHORBOL-ESTER BINDING
1351	1fmk		286	401	1.2e-26	0.33	0.16		TYROSINE-PROTEIN KINASE SRC; CHAIN: NULL;	PHOSPHOTRANSFERASE C-SRC, P60-SRC; SRC, TYROSINE KINASE, PHOSPHORYLATION, SH2, SH3, 2 PHOSPHOTYROSINE, PROTO-ONCOGENE, PHOSPHOTRANSFERASE
1351	1fyn	A	286	341	1.5e-19	0.26	0.69		PHOSPHOTRANSFERASE FYN; CHAIN: A; 3BP-2; CHAIN: B;	TRANSFERASE PROTO-ONCOGENE TYROSINE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										KINASE; PROTO-ONCOGENE, TRANSFERASE, TYROSINE-PROTEIN KINASE, 2 PHOSPHORYLATION, ATP-BINDING, MYRISTYLATION, SH3 DOMAIN, 3 COMPLEX (PHOSPHOTRANSFERASE/PEPTIDE)
1351	1gfc		288	341	1.5e-19	-0.17	1.00		ADAPTOR PROTEIN CONTAINING SH2 AND SH3 GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2 (GRB2) 1GFC 3 (C-TERMINAL SH3 DOMAIN) (NMR, MINIMIZED MEAN STRUCTURE) 1GFC 4	
1351	1gri	A	133	345	2.4e-13			65.01	GROWTH FACTOR BOUND PROTEIN 2; 1GRI 5 CHAIN: A, B; 1GRI 6	SIGNAL TRANSDUCTION ADAPTOR SH2, SH3 1GRI 14
1351	1gri	A	283	341	5.1e-20	0.07	0.84		GROWTH FACTOR BOUND PROTEIN 2; 1GRI 5 CHAIN: A, B; 1GRI 6	SIGNAL TRANSDUCTION ADAPTOR SH2, SH3 1GRI 14
1351	1gri	A	289	397	1.7e-23	-0.06	0.05		GROWTH FACTOR BOUND PROTEIN 2; 1GRI 5 CHAIN: A, B; 1GRI 6	SIGNAL TRANSDUCTION ADAPTOR SH2, SH3 1GRI 14
1351	1hsq		282	348	3.4e-17	0.52	0.31		PHOSPHORIC DIESTER HYDROLASE PHOSPHOLIPASE C-GAMMA (SH3 DOMAIN) (E.C.3.1.4.11) 1HSQ 3 (NMR, MINIMIZED MEAN STRUCTURE) 1HSQ 4	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1351	1lck	A	289	401	5.1e-22	0.35	0.13		P56=LCK= TYROSINE KINASE; 1LCK 7 CHAIN: A; 1LCK 8 TAIL PHOSPHOPEPTIDE TEGQ(PHOSPHO)YQPQA; 1LCK 14 CHAIN: B; 1LCK 15	COMPLEX (KINASE/PEPTIDE)
1351	1nlo	C	288	340	8.5e-18	0.44	0.98		C-SRC; CHAIN: C; NL1 (MN7-MN2-MN1-PLPLP); CHAIN: N;	COMPLEX (TRANSFERASE/PEPTIDE) SRC, SH3 DOMAIN, LIGANDS, NON-PEPTIDE ELEMENTS, 2 COMPLEX (TRANSFERASE/PEPTIDE)
1351	1ptq		103	152	3.4e-19	0.08	0.23		PROTEIN KINASE C DELTA TYPE; 1PTQ 4	PHOSPHOTRANSFERASE
1351	1ptq		176	209	5.1e-11	0.09	-0.20		PROTEIN KINASE C DELTA TYPE; 1PTQ 4	PHOSPHOTRANSFERASE
1351	1pwt		286	341	3.4e-15	0.08	0.99		ALPHA SPECTRIN; CHAIN: NULL;	CIRCULAR PERMUTANT PWT; CIRCULAR PERMUTANT, SH3 DOMAIN, CYTOSKELETON
1351	1pwt		289	341	2.4e-15	0.57	0.98		ALPHA SPECTRIN; CHAIN: NULL;	CIRCULAR PERMUTANT PWT; CIRCULAR PERMUTANT, SH3 DOMAIN, CYTOSKELETON
1351	1qcf	A	289	401	3.4e-26	0.27	0.30		HAEMATOPHOETIC CELL KINASE (HCK); CHAIN: A;	TYROSINE KINASE TYROSINE KINASE-INHIBITOR COMPLEX, DOWN-REGULATED KINASE, 2 ORDERED ACTIVATION LOOP
1351	1qkw	A	289	341	2.4e-15	0.19	0.89		ALPHA II SPECTRIN; CHAIN: A;	CYTOSKELETON CYTOSKELETON,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1351	1qly	A	286	340	1.7e-16	-0.56	0.96		TYROSINE-PROTEIN KINASE BTK; CHAIN: A;	MEMBRANE, SH3 DOMAIN TYROSINE-PROTEIN KINASE BRUTONS TYROSINE KINASE, B CELL PROGENITOR KINASE, TRANSFERASE, TYROSINE-PROTEIN KINASE, PHOSPHORYLATION, 2 SH3 DOMAIN
1351	1sem	A	289	338	8.5e-19	0.27	0.99		SEM-5; 1SEM 3 CHAIN: A, B; 1SEM 5 10-RESIDUE PROLINE-RICH PEPTIDE FROM MSOS 1SEM 8 CHAIN: C, D 1SEM 10	SIGNAL TRANSDUCTION PROTEIN SRC-HOMOLOGY 3 (SH3) DOMAIN, PEPTIDE-BINDING PROTEIN, 1SEM 18 2 GUANINE NUCLEOTIDE EXCHANGE FACTOR 1SEM 19
1351	1shf	A	286	341	1.5e-19	0.37	0.94		PHOSPHOTRANSFERASE FYN PROTO-ONCOGENE TYROSINE KINASE (E.C.2.7.1.112) 1SHF 3 (SH3 DOMAIN) 1SHF 4	
1351	2abl		281	398	1.7e-23	0.06	0.05		ABL TYROSINE KINASE; CHAIN: NULL;	TRANSFERASE TRANSFERASE, TYROSINE KINASE, SH3, SH2, ONCOPROTEIN
1351	4hck		289	341	5.1e-16	0.44	1.00		HEMATOPOIETIC CELL KINASE; CHAIN: NULL;	TRANSFERASE HCK; SH3, PROTEIN TYROSINE KINASE, SIGNAL TRANSDUCTION, 2 TRANSFERASE
1352	1ak2		292	357	4.8e-22	0.11	1.00		ADENYLATE KINASE	PHOSPHOTRANSFERASE



Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									ISOENZYM-2; CHAIN: NULL;	ATP\AMP PHOSPHOTRANSFERASE, MYOKINASE; NUCLEOSIDE MONOPHOSPHATE KINASE, PHOSPHOTRANSFERASE
1352	1ak2		292	357	4.8e-22	0.11	1.00		ADENYLATE KINASE ISOENZYM-2; CHAIN: NULL;	PHOSPHOTRANSFERASE ATP\AMP PHOSPHOTRANSFERASE, MYOKINASE; NUCLEOSIDE MONOPHOSPHATE KINASE, PHOSPHOTRANSFERASE
1352	1ak2		295	357	1.7e-14	0.06	1.00		ADENYLATE KINASE ISOENZYM-2; CHAIN: NULL;	PHOSPHOTRANSFERASE ATP\AMP PHOSPHOTRANSFERASE, MYOKINASE; NUCLEOSIDE MONOPHOSPHATE KINASE, PHOSPHOTRANSFERASE
1352	1ak2		295	357	1.7e-14	0.06	1.00		ADENYLATE KINASE ISOENZYM-2; CHAIN: NULL;	PHOSPHOTRANSFERASE ATP\AMP PHOSPHOTRANSFERASE, MYOKINASE; NUCLEOSIDE MONOPHOSPHATE KINASE, PHOSPHOTRANSFERASE
1352	1ak2		47	232	1.7e-36	0.49	1.00		ADENYLATE KINASE ISOENZYM-2; CHAIN: NULL;	PHOSPHOTRANSFERASE ATP\AMP PHOSPHOTRANSFERASE, MYOKINASE; NUCLEOSIDE MONOPHOSPHATE KINASE, PHOSPHOTRANSFERASE
1352	1ak2		47	232	1.7e-36	0.49	1.00		ADENYLATE KINASE ISOENZYM-2; CHAIN: NULL;	PHOSPHOTRANSFERASE ATP\AMP

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										PHOSPHOTRANSFERASE, MYOKINASE; NUCLEOSIDE MONOPHOSPHATE KINASE, PHOSPHOTRANSFERASE
1352	1ak2		47	233	2.4e-46	0.55	1.00		ADENYLATE KINASE ISOENZYME-2; CHAIN: NULL;	PHOSPHOTRANSFERASE ATP\AMP PHOSPHOTRANSFERASE, MYOKINASE; NUCLEOSIDE MONOPHOSPHATE KINASE, PHOSPHOTRANSFERASE
1352	1ak2		47	233	2.4e-46	0.55	1.00		ADENYLATE KINASE ISOENZYME-2; CHAIN: NULL;	PHOSPHOTRANSFERASE ATP\AMP PHOSPHOTRANSFERASE, MYOKINASE; NUCLEOSIDE MONOPHOSPHATE KINASE, PHOSPHOTRANSFERASE
1352	1ak2		47	237	2.4e-46			88.15	ADENYLATE KINASE ISOENZYME-2; CHAIN: NULL;	PHOSPHOTRANSFERASE ATP\AMP PHOSPHOTRANSFERASE, MYOKINASE; NUCLEOSIDE MONOPHOSPHATE KINASE, PHOSPHOTRANSFERASE
1352	1ak2		47	237	2.4e-46			88.15	ADENYLATE KINASE ISOENZYME-2; CHAIN: NULL;	PHOSPHOTRANSFERASE ATP\AMP PHOSPHOTRANSFERASE, MYOKINASE; NUCLEOSIDE MONOPHOSPHATE KINASE, PHOSPHOTRANSFERASE
1352	1aky		296	357	2.4e-21	0.51	1.00		ADENYLATE KINASE; 1AKY 4 CHAIN: NULL; 1AKY 5	TRANSFERASE (PHOSPHOTRANSFERASE) ATP\AMP

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										PHOSPHOTRANSFERASE, MYOKINASE; 1AKY 6 ATP:AMP PHOSPHOTRANSFERASE, MYOKINASE 1AKY 15
1352	1aky		296	357	2.4e-21	0.51	1.00		ADENYLATE KINASE; 1AKY 4 CHAIN: NULL; 1AKY 5	TRANSFERASE (PHOSPHOTRANSFERASE) ATP:AMP PHOSPHOTRANSFERASE, MYOKINASE; 1AKY 6 ATP:AMP PHOSPHOTRANSFERASE, MYOKINASE 1AKY 15
1352	1aky		48	235	1.1e-45			85.07	ADENYLATE KINASE; 1AKY 4 CHAIN: NULL; 1AKY 5	TRANSFERASE (PHOSPHOTRANSFERASE) ATP:AMP PHOSPHOTRANSFERASE, MYOKINASE; 1AKY 6 ATP:AMP PHOSPHOTRANSFERASE, MYOKINASE 1AKY 15
1352	1aky		48	235	1.1e-45			85.07	ADENYLATE KINASE; 1AKY 4 CHAIN: NULL; 1AKY 5	TRANSFERASE (PHOSPHOTRANSFERASE) ATP:AMP PHOSPHOTRANSFERASE, MYOKINASE; 1AKY 6 ATP:AMP PHOSPHOTRANSFERASE, MYOKINASE 1AKY 15
1352	1aky		49	233	1.1e-45	0.86	1.00		ADENYLATE KINASE; 1AKY 4 CHAIN: NULL; 1AKY 5	TRANSFERASE (PHOSPHOTRANSFERASE)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										ATP:AMP PHOSPHOTRANSFERASE, MYOKINASE; 1AKY 6 ATP:AMP PHOSPHOTRANSFERASE, MYOKINASE 1AKY 15
1352	1aky		49	233	1.1e-45	0.86	1.00		ADENYLATE KINASE; 1AKY 4 CHAIN: NULL; 1AKY 5	TRANSFERASE (PHOSPHOTRANSFERASE) ATP:AMP PHOSPHOTRANSFERASE, MYOKINASE; 1AKY 6 ATP:AMP PHOSPHOTRANSFERASE, MYOKINASE 1AKY 15
1352	1e4v	A	294	358	1.7e-14	0.05	1.00		ADENYLATE KINASE; CHAIN: A;	TRANSFERASE(PHOSPHOTR ANSFERASE) TRANSFERASE(PHOSPHOTR ANSFERASE)
1352	1e4v	A	294	358	1.7e-14	0.05	1.00		ADENYLATE KINASE; CHAIN: A;	TRANSFERASE(PHOSPHOTR ANSFERASE) TRANSFERASE(PHOSPHOTR ANSFERASE)
1352	1e4v	A	295	357	1.2e-21	0.31	1.00		ADENYLATE KINASE; CHAIN: A;	TRANSFERASE(PHOSPHOTR ANSFERASE) TRANSFERASE(PHOSPHOTR ANSFERASE)
1352	1e4v	A	295	357	1.2e-21	0.31	1.00		ADENYLATE KINASE; CHAIN: A;	TRANSFERASE(PHOSPHOTR ANSFERASE) TRANSFERASE(PHOSPHOTR ANSFERASE)
1352	1e4v	A	51	228	2.4e-46	0.41	1.00		ADENYLATE KINASE; CHAIN:	TRANSFERASE(PHOSPHOTR

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									A;	ANSFERASE) TRANSFERASE(PHOSPHOTR ANSFERASE)
1352	1e4v	A	51	228	2.4e-46	0.41	1.00		ADENYLATE KINASE; CHAIN: A;	TRANSFERASE(PHOSPHOTR ANSFERASE) TRANSFERASE(PHOSPHOTR ANSFERASE)
1352	1e4v	A	51	232	5.1e-33	0.40	1.00		ADENYLATE KINASE; CHAIN: A;	TRANSFERASE(PHOSPHOTR ANSFERASE) TRANSFERASE(PHOSPHOTR ANSFERASE)
1352	1e4v	A	51	232	5.1e-33	0.40	1.00		ADENYLATE KINASE; CHAIN: A;	TRANSFERASE(PHOSPHOTR ANSFERASE) TRANSFERASE(PHOSPHOTR ANSFERASE)
1352	1fzq	A	51	78	0.0073	-0.82	0.17		ADP-RIBOSYLATION FACTOR- LIKE PROTEIN 3; CHAIN: A;	SIGNALING PROTEIN ARF- LIKE PROTEIN 3, ARL3; PROTEIN-GDP COMPLEX WITHOUT MAGNESIUM, ARF FAMILY, RAS 2 SUPERFAMILY, G-DOMAIN
1352	1fzq	A	51	78	0.0073	-0.82	0.17		ADP-RIBOSYLATION FACTOR- LIKE PROTEIN 3; CHAIN: A;	SIGNALING PROTEIN ARF- LIKE PROTEIN 3, ARL3; PROTEIN-GDP COMPLEX WITHOUT MAGNESIUM, ARF FAMILY, RAS 2 SUPERFAMILY, G-DOMAIN
1352	1qf9	A	44	232	1.7e-37	0.90	1.00		URIDYLMONOPHOSPHATE/CYT IDYLMONOPHOSPHATE KINASE; CHAIN: A;	KINASE UMP/CMP KINASE; NUCLEOSIDE MONOPHOSPHATE KINASE, NMP KINASE, PHOSPHORYL

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										2 TRANSFER, TRANSITION STATE ANALOG COMPLEX, TRANSFERASE
1352	1qf9	A	44	232	1.7e-37	0.90	1.00		URIDYLMONOPHOSPHATE/CYT IDYLMONOPHOSPHATE KINASE; CHAIN: A;	KINASE UMP/CMP KINASE; NUCLEOSIDE MONOPHOSPHATE KINASE, NMP KINASE, PHOSPHORYL 2 TRANSFER, TRANSITION STATE ANALOG COMPLEX, TRANSFERASE
1352	1qf9	A	44	237	1.7e-37			141.35	URIDYLMONOPHOSPHATE/CYT IDYLMONOPHOSPHATE KINASE; CHAIN: A;	KINASE UMP/CMP KINASE; NUCLEOSIDE MONOPHOSPHATE KINASE, NMP KINASE, PHOSPHORYL 2 TRANSFER, TRANSITION STATE ANALOG COMPLEX, TRANSFERASE
1352	1qf9	A	44	237	1.7e-37			141.35	URIDYLMONOPHOSPHATE/CYT IDYLMONOPHOSPHATE KINASE; CHAIN: A;	KINASE UMP/CMP KINASE; NUCLEOSIDE MONOPHOSPHATE KINASE, NMP KINASE, PHOSPHORYL 2 TRANSFER, TRANSITION STATE ANALOG COMPLEX, TRANSFERASE
1352	1ukz		292	357	1.5e-11	-0.19	0.89		TRANSFERASE URIDYLATE KINASE (E.C.2.7.4.-) COMPLEXED WITH ADP AND AMP 1UKZ 3	
1352	1ukz		292	357	1.5e-11	-0.19	0.89		TRANSFERASE URIDYLATE KINASE (E.C.2.7.4.-) COMPLEXED WITH ADP AND	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									AMP 1UKZ 3	
1352	1ukz		44	236	1.2e-37			158.82	TRANSFERASE URIDYLATE KINASE (E.C.2.7.4.-) COMPLEXED WITH ADP AND AMP 1UKZ 3	
1352	1ukz		44	236	1.2e-37			158.82	TRANSFERASE URIDYLATE KINASE (E.C.2.7.4.-) COMPLEXED WITH ADP AND AMP 1UKZ 3	
1352	1ukz		44	236	1.2e-37	0.91	1.00		TRANSFERASE URIDYLATE KINASE (E.C.2.7.4.-) COMPLEXED WITH ADP AND AMP 1UKZ 3	
1352	1ukz		44	236	1.2e-37	0.91	1.00		TRANSFERASE URIDYLATE KINASE (E.C.2.7.4.-) COMPLEXED WITH ADP AND AMP 1UKZ 3	
1352	1ukz		51	232	5.1e-35	0.76	1.00		TRANSFERASE URIDYLATE KINASE (E.C.2.7.4.-) COMPLEXED WITH ADP AND AMP 1UKZ 3	
1352	1ukz		51	232	5.1e-35	0.76	1.00		TRANSFERASE URIDYLATE KINASE (E.C.2.7.4.-) COMPLEXED WITH ADP AND AMP 1UKZ 3	
1352	1zak	A	291	359	6.8e-15	0.32	1.00		ADENYLATE KINASE; CHAIN: A, B;	TRANSFERASE ATP:AMP-PHOSPHOTRANSFERASE, TRANSFERASE
1352	1zak	A	291	359	6.8e-15	0.32	1.00		ADENYLATE KINASE; CHAIN: A, B;	TRANSFERASE ATP:AMP-PHOSPHOTRANSFERASE, TRANSFERASE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1352	1zak	A	47	246	8.5e-33			95.58	ADENYLATE KINASE; CHAIN: A, B;	TRANSFERASE ATP:AMP-PHOSPHOTRANSFERASE, TRANSFERASE
1352	1zak	A	47	246	8.5e-33			95.58	ADENYLATE KINASE; CHAIN: A, B;	TRANSFERASE ATP:AMP-PHOSPHOTRANSFERASE, TRANSFERASE
1352	1zin		294	358	1.7e-16	0.39	1.00		ADENYLATE KINASE; CHAIN: NULL;	PHOSPHOTRANSFERASE ADK; PHOSPHOTRANSFERASE, ZINC FINGER
1352	1zin		294	358	1.7e-16	0.39	1.00		ADENYLATE KINASE; CHAIN: NULL;	PHOSPHOTRANSFERASE ADK; PHOSPHOTRANSFERASE, ZINC FINGER
1352	1zin		51	236	3.4e-36			88.98	ADENYLATE KINASE; CHAIN: NULL;	PHOSPHOTRANSFERASE ADK; PHOSPHOTRANSFERASE, ZINC FINGER
1352	1zin		51	236	3.4e-36			88.98	ADENYLATE KINASE; CHAIN: NULL;	PHOSPHOTRANSFERASE ADK; PHOSPHOTRANSFERASE, ZINC FINGER
1352	1zin		53	232	3.4e-36	0.53	1.00		ADENYLATE KINASE; CHAIN: NULL;	PHOSPHOTRANSFERASE ADK; PHOSPHOTRANSFERASE, ZINC FINGER
1352	1zin		53	232	3.4e-36	0.53	1.00		ADENYLATE KINASE; CHAIN: NULL;	PHOSPHOTRANSFERASE ADK; PHOSPHOTRANSFERASE, ZINC FINGER
1352	2ak3	A	44	248	3.4e-28			86.82	TRANSFERASE	



Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									(PHOSPHOTRANSFERASE) ADENYLATE KINASE ISOENZYME-3 (GTP: AMP PHOSPHOTRANSFERASE) 2AK3 3 (E.C.2.7.4.10) 2AK3 4 TRANSFERASE	
1352	2ak3	A	44	248	3.4e-28			86.82	(PHOSPHOTRANSFERASE) ADENYLATE KINASE ISOENZYME-3 (GTP: AMP PHOSPHOTRANSFERASE) 2AK3 3 (E.C.2.7.4.10) 2AK3 4	
1352	2ng1		18	162	1e-08	0.04	-0.15		SIGNAL SEQUENCE RECOGNITION PROTEIN FFH; CHAIN: NULL;	SIGNAL RECOGNITION FFH; FFH, SRP, GTPASE, SIGNAL RECOGNITION PARTICLE, GDP
1352	2ng1		18	162	1e-08	0.04	-0.15		SIGNAL SEQUENCE RECOGNITION PROTEIN FFH; CHAIN: NULL;	SIGNAL RECOGNITION FFH; FFH, SRP, GTPASE, SIGNAL RECOGNITION PARTICLE, GDP
1352	3adk		287	358	2.4e-17	0.00	1.00		TRANSFERASE(PHOSPHOTRANSFERASE) ADENYLATE KINASE (E.C.2.7.4.3) 3ADK 4	
1352	3adk		287	358	2.4e-17	0.00	1.00		TRANSFERASE(PHOSPHOTRANSFERASE) ADENYLATE KINASE (E.C.2.7.4.3) 3ADK 4	
1352	3adk		291	357	6.8e-14	0.11	1.00		TRANSFERASE(PHOSPHOTRANSFERASE) ADENYLATE KINASE (E.C.2.7.4.3) 3ADK 4	
1352	3adk		291	357	6.8e-14	0.11	1.00		TRANSFERASE(PHOSPHOTRANSFERASE) ADENYLATE KINASE (E.C.2.7.4.3) 3ADK 4	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1352	3adk		42	236	5.1e-42			160.04	TRANSFERASE(PHOSPHOTRANSFERASE) ADENYLATE KINASE (E.C.2.7.4.3) 3ADK 4	
1352	3adk		42	236	5.1e-42			160.04	TRANSFERASE(PHOSPHOTRANSFERASE) ADENYLATE KINASE (E.C.2.7.4.3) 3ADK 4	
1352	3adk		43	232	5.1e-42	0.80	1.00		TRANSFERASE(PHOSPHOTRANSFERASE) ADENYLATE KINASE (E.C.2.7.4.3) 3ADK 4	
1352	3adk		43	232	5.1e-42	0.80	1.00		TRANSFERASE(PHOSPHOTRANSFERASE) ADENYLATE KINASE (E.C.2.7.4.3) 3ADK 4	
1358	1av1	A	90	291	6e-09			53.18	APOLIPOPROTEIN A-I; CHAIN: A, B, C, D;	LIPID TRANSPORT APO A-I; LIPOPROTEIN, LIPID TRANSPORT, CHOLESTEROL METABOLISM, 2 ATHEROSCLEROSIS, HDL, LCAT-ACTIVATION
1358	1cun	A	89	297	8.4e-09			55.89	ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1362	1a6b	B	14	42	0.0012	-0.47	0.06		DNA (5'-D(*AP*CP*GP*CP*C)-3'); CHAIN: A; ZINC FINGER PROTEIN NCP10; CHAIN: B;	COMPLEX (NUCLEOCAPSID PROTEIN/DNA) MOMULV; NUCLEOCAPSID PROTEIN,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1362	1bdq	A	42	136	3.4e-31	0.30	0.47		HIV-1 PROTEASE; CHAIN: A, B;	INTERCALATION, NUCLEIC ACID, 2 RETROVIRUS, ZINC FINGER
1362	1bwb	A	42	136	3.4e-32	0.34	0.19		HIV-1 PROTEASE; CHAIN: A, B;	HYDROLASE HYDROLASE, AIDS, POLYPROTEIN, ASPARTYL PROTEASE, ACID 2 PROTEASE, HYDROXYETHYLENE ISOSTERE INHIBITOR, SUBSTRATE 3 ANALOGUE INHIBITOR
1362	1c0t	A	169	765	0	-0.15	1.00		HIV-1 REVERSE TRANSCRIPTASE (A-CHAIN); CHAIN: A; HIV-1 REVERSE TRANSCRIPTASE (B-CHAIN); CHAIN: B;	HYDROLASE HIV-1 PROTEASE, HYDROLASE TRANSFERASE HIV-1 REVERSE TRANSCRIPTASE, AIDS, NON-NUCLEOSIDE INHIBITOR, 2 DRUG DESIGN
1362	1c0t	B	172	613	0	-0.14	0.48		HIV-1 REVERSE TRANSCRIPTASE (A-CHAIN); CHAIN: A; HIV-1 REVERSE TRANSCRIPTASE (B-CHAIN); CHAIN: B;	TRANSFERASE HIV-1 REVERSE TRANSCRIPTASE, AIDS, NON-NUCLEOSIDE INHIBITOR, 2 DRUG DESIGN
1362	1c1c	B	170	613	0	0.02	0.96		HIV-1 REVERSE TRANSCRIPTASE (A-CHAIN); CHAIN: A; HIV-1 REVERSE TRANSCRIPTASE (B-CHAIN); CHAIN: B;	TRANSFERASE HIV-1 REVERSE TRANSCRIPTASE, AIDS, NON-NUCLEOSIDE INHIBITOR, 2 DRUG DESIGN
1362	1c9r	A	166	783	0			153.92	HIV-1 REVERSE TRANSCRIPTASE (CHAIN A); CHAIN: A; HIV-1 REVERSE	TRANSFERASE/IMMUNE SYSTEM/DNA HIV-1 RT; HIV-1 RT; HIV, REVERSE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									TRANSCRIPTASE (CHAIN B); CHAIN: B; ANTIBODY (LIGHT CHAIN); CHAIN: L; ANTIBODY (HEAVY CHAIN); CHAIN: H; DNA (5'- CHAIN: T; DNA (5'- CHAIN: P;	TRANSCRIPTASE, MET184ILE, 3TC, PROTEIN-DNA 2 COMPLEX, DRUG RESISTANCE, M184I, TRANSFERASE/IMMUNE 3 SYSTEM/DNA
1362	1c9r	A	166	787	0	0.01	1.00		HIV-1 REVERSE TRANSCRIPTASE (CHAIN A); CHAIN: A; HIV-1 REVERSE TRANSCRIPTASE (CHAIN B); CHAIN: B; ANTIBODY (LIGHT CHAIN); CHAIN: L; ANTIBODY (HEAVY CHAIN); CHAIN: H; DNA (5'- CHAIN: T; DNA (5'- CHAIN: P;	TRANSFERASE/IMMUNE SYSTEM/DNA HIV-1 RT; HIV-1 RT; HIV, REVERSE TRANSCRIPTASE, MET184ILE, 3TC, PROTEIN-DNA 2 COMPLEX, DRUG RESISTANCE, M184I, TRANSFERASE/IMMUNE 3 SYSTEM/DNA
1362	1c9r	B	166	585	0			125.58	HIV-1 REVERSE TRANSCRIPTASE (CHAIN A); CHAIN: A; HIV-1 REVERSE TRANSCRIPTASE (CHAIN B); CHAIN: B; ANTIBODY (LIGHT CHAIN); CHAIN: L; ANTIBODY (HEAVY CHAIN); CHAIN: H; DNA (5'- CHAIN: T; DNA (5'- CHAIN: P;	TRANSFERASE/IMMUNE SYSTEM/DNA HIV-1 RT; HIV-1 RT; HIV, REVERSE TRANSCRIPTASE, MET184ILE, 3TC, PROTEIN-DNA 2 COMPLEX, DRUG RESISTANCE, M184I, TRANSFERASE/IMMUNE 3 SYSTEM/DNA
1362	1c9r	B	166	613	0	-0.21	0.76		HIV-1 REVERSE TRANSCRIPTASE (CHAIN A); CHAIN: A; HIV-1 REVERSE TRANSCRIPTASE (CHAIN B); CHAIN: B; ANTIBODY (LIGHT CHAIN); CHAIN: L; ANTIBODY (HEAVY CHAIN); CHAIN: H;	TRANSFERASE/IMMUNE SYSTEM/DNA HIV-1 RT; HIV-1 RT; HIV, REVERSE TRANSCRIPTASE, MET184ILE, 3TC, PROTEIN-DNA 2 COMPLEX, DRUG RESISTANCE, M184I,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1362	1daz	C	42	136	8.5e-31	0.33	0.35		DNA (5'-CHAIN: T; DNA (5'-CHAIN: P; PEPTIDE INHIBITOR; CHAIN: A, B; HIV-1 PROTEASE (RETROPEPSIN); CHAIN: C, D; OCCUPANCY	TRANSFERASE/IMMUNE 3 SYSTEM/DNA
1362	1f21	A	651	790	3.4e-16	0.44	0.89		RIBONUCLEASE HI; CHAIN: A;	HYDROLASE RNASE H, NUCLEASE, RNASE H*, RIBONUCLEASE H, METAL-BINDING 2 PROTEIN, PROTEIN FOLDING
1362	1f21	A	651	794	2.4e-26	0.61	1.00		RIBONUCLEASE HI; CHAIN: A;	HYDROLASE RNASE H, NUCLEASE, RNASE H*, RIBONUCLEASE H, METAL-BINDING 2 PROTEIN, PROTEIN FOLDING
1362	1g6l	A	38	136	8.5e-33	0.27	0.54		HIV-1 PROTEASE; CHAIN: A;	HYDROLASE HYDROLASE
1362	1g6l	A	42	189	1.4e-32	-0.03	0.05		HIV-1 PROTEASE; CHAIN: A;	HYDROLASE HYDROLASE
1362	1hrh	A	638	787	3.4e-22	0.13	0.46		HYDROLASE(ENDORIBONUCLEASE) RIBONUCLEASE H DOMAIN OF /HIV-1\$ REVERSE TRANSCRIPTASE 1HRH 3	
1362	1hvc		42	189	6.8e-33	-0.04	0.09		HYDROLASE(ACID PROTEASE) HIV-1 PROTEASE (TETHERED DIMER LINKED BY 1HVC 3 GLY-SER-SER-GLY) COMPLEXED WITH A-76928 1HVC 4	
1362	1ida	A	42	136	1.7e-20	0.39	0.11		HYDROLASE(ACID PROTEINASE) HUMAN IMMUNODEFICIENCY VIRUS	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									TYPE 2 (HIV-2) PROTEASE IIDA 3 COMPLEXED WITH THE INHIBITOR BILA 1906 CONTAINING THE IIDA 4 HYDROXYETHYLAMINE DIPEPTIDE ISOSTERE IIDA 5	
1362	1mml		150	392	5.1e-67	0.70	1.00		MMLV REVERSE TRANSCRIPTASE; IMML 4 CHAIN: NULL; IMML 5	REVERSE TRANSCRIPTASE
1362	1mml		151	393	5.1e-67			204.88	MMLV REVERSE TRANSCRIPTASE; IMML 4 CHAIN: NULL; IMML 5	REVERSE TRANSCRIPTASE
1362	1mtr	A	42	134	8.5e-30	0.25	0.63		HIV-1 PROTEASE; A CYCLIC PHE-ILE-VAL PEPTIDOMIMETIC INHIBITOR; CHAIN: C;	COMPLEX (ASPARTYL PROTEASE/INHIBITOR) HIV-1 PR; HYDROLASE, ASPARTYL PROTEINASE, AIDS, PEPTIDE, INHIBITOR
1362	1ril		651	784	5.1e-11	0.16	0.43		HYDROLASE(ENDORIBONUCLEASE) RIBONUCLEASE H (E.C.3.1.26.4) 1RIL 3	
1362	1ril		651	787	4.8e-25	0.36	1.00		HYDROLASE(ENDORIBONUCLEASE) RIBONUCLEASE H (E.C.3.1.26.4) 1RIL 3	
1362	1rth	A	166	768	0	-0.05	1.00		HIV-1 REVERSE TRANSCRIPTASE; 1RTH 4 CHAIN: A, B; 1RTH 5	NUCLEOTIDYLTRANSFERASE HIV-1 RT; 1RTH 6 HIV-1 REVERSE TRANSCRIPTASE 1RTH 15
1362	1rth	A	166	769	0			152.40	HIV-1 REVERSE TRANSCRIPTASE; 1RTH 4 CHAIN: A, B; 1RTH 5	NUCLEOTIDYLTRANSFERASE HIV-1 RT; 1RTH 6 HIV-1 REVERSE TRANSCRIPTASE 1RTH 15

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1362	1rth	B	168	602	0			128.83	HIV-1 REVERSE TRANSCRIPTASE; 1RTH 4 CHAIN: A, B; 1RTH 5	NUCLEOTIDYLTRANSFERASE HIV-1 RT; 1RTH 6 HIV-1 REVERSE TRANSCRIPTASE 1RTH 15
1362	1rth	B	168	613	0	-0.01	0.93		HIV-1 REVERSE TRANSCRIPTASE; 1RTH 4 CHAIN: A, B; 1RTH 5	NUCLEOTIDYLTRANSFERASE HIV-1 RT; 1RTH 6 HIV-1 REVERSE TRANSCRIPTASE 1RTH 15
1362	1sip		42	136	3.4e-21	0.38	0.27		HYDROLASE(ACID PROTEINASE) SIMIAN IMMUNODEFICIENCY VIRUS (SIV) PROTEINASE 1SIP 3 (SIV MAC251-32H ISOLATE) (E.C.3.4.23.-) 1SIP 4	
1362	1vrt	A	169	712	0			156.57	HIV-1 REVERSE TRANSCRIPTASE; 1VRT 4 CHAIN: A, B; 1VRT 5	NUCLEOTIDYLTRANSFERASE HIV-1 RT; 1VRT 6 HIV-1 REVERSE TRANSCRIPTASE 1VRT 15
1362	1vrt	A	169	765	0	0.00	1.00		HIV-1 REVERSE TRANSCRIPTASE; 1VRT 4 CHAIN: A, B; 1VRT 5	NUCLEOTIDYLTRANSFERASE HIV-1 RT; 1VRT 6 HIV-1 REVERSE TRANSCRIPTASE 1VRT 15
1362	1vrt	B	170	583	0			125.02	HIV-1 REVERSE TRANSCRIPTASE; 1VRT 4 CHAIN: A, B; 1VRT 5	NUCLEOTIDYLTRANSFERASE HIV-1 RT; 1VRT 6 HIV-1 REVERSE TRANSCRIPTASE 1VRT 15
1362	1vrt	B	170	613	0	-0.05	0.90		HIV-1 REVERSE TRANSCRIPTASE; 1VRT 4 CHAIN: A, B; 1VRT 5	NUCLEOTIDYLTRANSFERASE HIV-1 RT; 1VRT 6 HIV-1 REVERSE TRANSCRIPTASE 1VRT 15
1362	2hvp		42	136	1e-32	0.14	0.31		RECORD./HIV\$-1 PROTEASE	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									2HVP 4	
1362	3hvt	B	167	583	0			123.43	NUCLEOTIDYLTRANSFERASE REVERSE TRANSCRIPTASE (E.C.2.7.7.49) 3HVT 3	
1362	3hvt	B	167	613	0	-0.15	0.94		NUCLEOTIDYLTRANSFERASE REVERSE TRANSCRIPTASE (E.C.2.7.7.49) 3HVT 3	
1367	1alh	A	263	343	1e-26	0.17	-0.11		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1367	1alh	A	291	371	1.7e-27	0.27	0.29		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1367	1alh	A	293	400	4.8e-30	-0.04	0.36		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1367	1ext	A	452	614	0.00072	0.30	0.00		TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	SIGNALLING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALLING PROTEIN
1367	1mey	C	181	259	1.7e-30	-0.47	0.16		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN



Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1367	1mey	C	210	287	1.7e-37	-0.02	0.29		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1367	1mey	C	237	315	3.4e-41	0.21	0.18		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1367	1mey	C	262	343	1e-44	0.27	0.17		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1367	1mey	C	290	371	1.2e-45	0.27	0.64		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1367	1mey	C	290	399	3.6e-29	0.01	0.21		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1367	1mey	C	318	399	6.8e-47	0.34	0.90		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1367	1mey	C	346	427	1e-47	0.24	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1367	1mey	C	374	455	5.1e-48	0.63	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1367	1mey	C	402	483	1.7e-47	0.51	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1367	1mey	C	402	484	5.1e-48			102.78	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1367	1mey	C	430	511	5.1e-48	0.93	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1367	1mey	C	458	539	5.1e-48	0.44	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1367	1mey	C	458	566	2.4e-41	0.00	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1367	1mey	C	486	566	5.1e-46	0.40	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	(ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1367	1mey	C	542	622	1.7e-46	0.52	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1367	1mey	C	569	650	3.4e-49	0.25	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1367	1mey	C	597	678	1.7e-49	0.47	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1367	1mey	C	625	706	3.4e-50	0.58	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER	COMPLEX (ZINC FINGER/DNA) ZINC FINGER,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									PROTEIN; CHAIN: C, F, G;	PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1367	1mey	C	681	762	1.7e-50	0.49	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1367	1mey	C	709	790	3.4e-50	0.74	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1367	1mey	C	737	818	3.4e-50	0.71	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1367	1mey	C	765	825	3.4e-36	0.28	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1367	1mey	G	208	235	6.8e-08	-0.17	0.12		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	STRUCTURE, COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1367	1mey	G	540	566	3.4e-10	0.87	0.99		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1367	1mey	G	540	566	9.6e-13	0.87	0.99		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1367	1ff6	A	238	427	2.4e-41	-0.25	0.10		TFIIIA; CHAIN: A, D, 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1367	1tf6	A	263	408	1.4e-34	-0.08	0.28		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1367	1tf6	A	319	469	3.4e-36	0.32	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1367	1tf6	A	375	520	1.7e-36	0.40	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1367	1tf6	A	375	594	6e-71	-0.26	0.51		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1367	1tf6	A	430	588	6e-71			106.93	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	PROTEIN COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1367	1tf6	A	431	575	1.7e-36	0.30	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1367	1tf6	A	543	687	1.5e-37	0.25	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1367	1tf6	A	570	715	3.4e-38	0.13	0.98		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION



Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										INITIATION, ZINC FINGER PROTEIN
1367	1tf6	A	570	734	4.8e-71	0.13	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1367	1tf6	A	626	790	9.6e-72	0.28	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1367	1tf6	A	682	820	1e-36	0.44	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1367	1tf6	A	682	825	2.4e-61	0.43	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1367	1ubd	C	245	343	5.1e-30	0.06	-0.12		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1367	1ubd	C	293	399	3.4e-32	0.30	0.70		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1367	1ubd	C	316	427	8.4e-43	0.03	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1367	1ubd	C	326	427	6.8e-33	0.09	1.00		YY1; CHAIN: C; ADENO-	COMPLEX (TRANSCRIPTION REGULATION/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1367	1ubd	C	354	455	1.2e-33	0.28	1.00		YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1367	1ubd	C	372	483	9.6e-55	0.19	1.00		YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1367	1ubd	C	410	511	1.7e-33	0.87	1.00		YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1367	1ubd	C	428	566	6e-52	0.03	0.95		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1367	1ubd	C	438	539	1.5e-33	0.33	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1367	1ubd	C	484	594	9.6e-53	0.29	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1367	1ubd	C	494	594	1.4e-32	0.26	1.00		YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1367	1ubd	C	540	650	2.4e-55	0.23	1.00		YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1367	1ubd	C	549	650	1e-34	0.25	1.00		YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1367	1ubd	C	577	678	5.1e-35	0.15	1.00		YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1367	1ubd	C	595	706	6e-54	0.29	1.00		YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1367	1ubd	C	633	734	3.4e-35	0.43	1.00		YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1367	1ubd	C	651	762	6e-52	0.33	1.00		YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1367	1ubd	C	686	790	3.4e-34	0.56	1.00		YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1367	1ubd	C	707	818	1.1e-53	0.38	1.00		YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1367	1ubd	C	717	818	5.1e-35	0.28	1.00		YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1367	2gli	A	119	258	1.4e-19	-0.16	0.49		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1367	2gli	A	238	429	1.1e-43	-0.07	0.53		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1367	2gli	A	262	398	8.5e-32	0.23	0.21		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1367	2gli	A	290	485	1.2e-55	0.17	0.95		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1367	2gli	A	354	482	1e-32	0.59	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1367	2gli	A	375	513	1.2e-68	0.66	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1367	2gli	A	458	624	1.2e-70	0.22	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)



Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1367	2gli	A	466	593	3.4e-33	0.66	0.92		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	BINDING PROTEIN/DNA)
1367	2gli	A	522	649	3.4e-34	0.24	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1367	2gli	A	542	708	1.2e-71	0.27	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1367	2gli	A	625	820	9.6e-68	0.29	0.96		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1367	2gli	A	689	820	1e-34	0.46	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1369	1a4y	A	322	750	5.1e-41	0.10	0.90		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE),

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS
1369	1a4y	A	403	865	3.4e-60			260.73	RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS
1369	1a4y	A	481	864	3.4e-60	0.68	1.00		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS
1369	1a4y	A	558	861	2e-78	0.84	1.00		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1369	1a9n	A	531	644	3.4e-07	0.13	0.37		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	REPEATS COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1369	1a9n	A	634	750	0.0015	0.40	0.19		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1369	1a9n	C	634	750	0.0015	0.59	0.13		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1369	1d0b	A	550	751	6.8e-19	0.03	0.24		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1369	1d0b	A	716	864	1.2e-10	-0.19	0.13		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1369	1dce	A	531	665	1.4e-11	0.06	-0.12		RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N-FORMYLMETHIONINE,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									D;	ALPHA SUBUNIT, BETA SUBUNIT
1369	1dce	A	602	703	1e-07	0.08	0.57		RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1369	1dce	A	770	861	3.4e-07	0.53	0.22		RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1369	1ds9	A	586	751	1.7e-08	0.03	-0.02		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1369	1ds9	A	700	843	1e-08	0.12	-0.14		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1369	1fo1	A	658	732	3.4e-06	-0.22	0.06		NUCLEAR RNA EXPORT	RNA BINDING PROTEIN TAP

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									FACTOR 1; CHAIN: A, B;	(NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
1369	1fo1	B	658	732	3.4e-06	-0.16	0.30		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
1369	1fqv	A	434	755	1.6e-08	-0.01	0.00		SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P;	LIGASE CYCLIN A/CDK2- ASSOCIATED PROTEIN P45; CYCLIN A/CDK2- ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
1369	1fqv	A	482	721	1e-13	0.00	-0.18		SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P;	LIGASE CYCLIN A/CDK2- ASSOCIATED PROTEIN P45; CYCLIN A/CDK2- ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
1369	1fs2	A	469	721	1.7e-14	0.05	-0.17		SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;	LIGASE CYCLIN A/CDK2- ASSOCIATED P45; CYCLIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										A/CDK2-ASSOCIATED P19; SKP1, SKP2, F-BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE
1369	1fs2	A	663	854	1e-13	0.05	-0.05		SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;	LIGASE CYCLIN A/CDK2-ASSOCIATED P45; CYCLIN A/CDK2-ASSOCIATED P19; SKP1, SKP2, F-BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE
1369	1yrg	A	480	751	8.5e-18	0.39	0.55		GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;	TRANSCRIPTION RNA1P; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SPI1, GTPASE-ACTIVATING PROTEIN, GAP, RNA1P, RANGAP, LRR, LEUCINE-2 RICH REPEAT PROTEIN, TWINNING, HEMIHERAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY
1369	1yrg	A	552	846	8.5e-20	0.48	0.89		GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;	TRANSCRIPTION RNA1P; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SPI1, GTPASE-ACTIVATING PROTEIN, GAP, RNA1P, RANGAP, LRR, LEUCINE-2 RICH REPEAT PROTEIN,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1369	1yrg	A	604	862	5.1e-16	0.65	0.94		GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;	TWINNING, HEMIHEDRAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY
1369	2bnh		322	750	3.4e-47	0.21	0.98		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	TRANSCRIPTION RNAIP; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SPI1, GTPASE-ACTIVATING PROTEIN, GAP, RNAIP, RANGAP, LRR, LEUCINE-2 RICH REPEAT PROTEIN, TWINNING, HEMIHEDRAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY
1369	2bnh		407	865	1.5e-65			259.80	RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGEN IN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
1369	2bnh		484	864	1.5e-65	0.65	1.00		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGEN IN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1384	1aye		4	110	1.7e-27	0.00	-0.11		PROCARBOXYPEPTIDASE A2; CHAIN: NULL;	SERINE PROTEASE PCPA2; SERINE PROTEASE, ZYMOGEN, HYDROLASE
1384	1cpb		2	110	3.4e-31	0.09	-0.02		HYDROLASE (C-TERMINAL PEPTIDASE) CARBOXYPEPTIDASE B (E.C.3.4.12.3) FRACTION II ICPB <sub>4</sub>	
1384	1did	A	4	110	3.4e-27	0.01	-0.07		CARBOXYPEPTIDASE A2; CHAIN: A; METALLOCARBOXYPEPTIDASE INHIBITOR; CHAIN: B	HYDROLASE/HYDROLASE INHIBITOR CARBOXYPEPTIDASE A2, LEECH CARBOXYPEPTIDASE INHIBITOR
1384	1obr		5	109	3.4e-24	-0.04	0.05		CARBOXYPEPTIDASE T; CHAIN: NULL;	HYDROLASE HYDROLASE, CARBOXYPEPTIDASE
1388	1bwz	A	57	343	5.1e-72	-0.22	0.21		DIAMINOPIMELATE EPIMERASE; CHAIN: A;	ISOMERASE DAP EPIMERASE; METABOLIC ROLE, STRUCTURAL CLASSIFICATION, ISOMERASE
1389	1a1h	A	454	552	8.5e-25	-0.29	0.06		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1389	1mey	C	117	198	3.4e-45	0.06	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER	COMPLEX (ZINC FINGER/DNA) ZINC FINGER,



Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									PROTEIN; CHAIN: C, F, G;	PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1389	1mey	C	117	198	3.6e-47	0.06	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1389	1mey	C	201	282	4.8e-49	0.21	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1389	1mey	C	201	282	8.5e-49	0.21	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1389	1mey	C	229	310	3.4e-49	0.24	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1389	1mey	C	257	338	1.2e-49	0.25	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	STRUCTURE, COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1389	1mey	C	285	366	1.7e-50	0.30	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1389	1mey	C	313	394	3.4e-50	0.01	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1389	1mey	C	33	114	3.4e-40	-0.17	0.45		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1389	1mey	C	341	422	3.4e-50	0.20	1.00		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1389	1mey	C	369	450	8.5e-51	0.07	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1389	1mey	C	397	478	1.2e-49	-0.02	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1389	1mey	C	397	479	8.5e-51			104.07	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1389	1mey	C	425	526	3.4e-44	-0.08	0.80		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1389	1mey	C	453	553	1.7e-44	-0.07	0.87		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1389	1mey	C	61	142	8.5e-42	-0.10	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1389	1mey	C	89	170	1.7e-43	-0.03	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1389	1mey	C	91	170	3.6e-45	-0.08	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1389	1mey	G	395	422	1.2e-13	0.19	0.90		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1389	1mey	G	395	422	1e-12	0.19	0.90		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1389	1mey	G	527	553	8.5e-12	-0.14	0.69		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1389	1tf6	A	117	278	8.4e-79			111.69	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1389	1tf6	A	118	282	8.4e-79	-0.14	0.78		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN:	COMPLEX (TRANSCRIPTION REGULATION/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1389	1tf6	A	174	319	1.7e-37	-0.03	0.52		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1389	1tf6	A	174	338	1.2e-76	0.05	0.71		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1389	1tf6	A	202	366	6e-76	0.03	0.74		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1389	1tf6	A	230	394	2.4e-74	-0.30	0.89		TFIIIA; CHAIN: A, D; 5S	COMPLEX (TRANSCRIPTION

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	REGULATION/DNA COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1389	1ff6	A	286	436	1.7e-37	0.05	0.90		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1389	1ff6	A	314	460	1e-37	-0.21	0.98		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1389	1ff6	A	342	488	5.1e-36	0.15	0.93		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1389	1tf6	A	370	553	3.6e-67	-0.35	0.48		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1389	1tf6	A	398	536	1.5e-32	-0.31	0.39		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1389	1tf6	A	62	207	1.7e-33	0.20	0.89		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1389	1tf6	A	71	226	8.4e-67	0.13	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER



Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1389	1tf6	A	91	254	7.2e-77	-0.15	0.86		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	PROTEIN COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1389	1ubd	C	143	254	7.2e-59	0.08	0.99		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1389	1ubd	C	199	310	1.2e-58	-0.15	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1389	1ubd	C	255	366	9.6e-55	0.01	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA- PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1389	1ubd	C	265	366	5.1e-36	-0.13	0.86		YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING- YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA- PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1389	1ubd	C	321	422	6.8e-35	-0.09	0.99		YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING- YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA- PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1389	1ubd	C	339	450	2.4e-55	-0.45	1.00		YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING- YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA- PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1389	1ubd	C	346	450	1.4e-35	0.05	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	REGULATION/DNA COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1389	1ubd	C	36	142	1e-27	-0.15	0.86		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1389	1ubd	C	371	479	2.4e-55			89.76	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1389	1ubd	C	395	526	8.4e-50	-0.34	0.49		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									CHAIN: A, B;	INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1389	1ubd	C	405	526	1.5e-32	-0.21	0.60		YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1389	1ubd	C	433	553	1.7e-29	-0.29	0.25		YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1389	1ubd	C	5	114	3.4e-27	-0.30	0.03		YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1389	1ubd	C	66	170	4.8e-46	-0.01	0.98		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1389	1ubd	C	87	198	3.6e-55	-0.03	0.99		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1389	1ubd	C	97	198	1.7e-31	-0.12	0.83		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1389	2gli	A	117	283	2.4e-75	-0.09	0.87		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1389	2gli	A	145	312	4.8e-75	0.13	0.86		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1389	2gli	A	201	340	2.4e-75			91.28	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1389	2gli	A	201	367	1.2e-71	-0.21	0.95		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1389	2gli	A	285	452	8.4e-72	-0.06	0.93		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1389	2gli	A	313	500	7.2e-71	-0.33	0.31		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1389	2gli	A	33	169	1e-29	-0.14	0.29		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1389	2gli	A	377	528	1e-31	-0.24	0.27		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1389	2gli	A	433	553	1.7e-30	-0.05	0.57		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1389	2gli	A	62	200	2.4e-59	-0.06	0.42		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1391	1bg2		1	237	1e-75			97.18	KINESIN; CHAIN: NULL;	MOTOR PROTEIN MOTOR PROTEIN, ATPASE, MICROTUBULE ASSOCIATED
1391	1bg2		1	237	1e-75	0.38	1.00		KINESIN; CHAIN: NULL;	MOTOR PROTEIN MOTOR PROTEIN, ATPASE, MICROTUBULE ASSOCIATED
1391	1bg2		1	237	3.4e-59	0.35	1.00		KINESIN; CHAIN: NULL;	MOTOR PROTEIN MOTOR PROTEIN, ATPASE, MICROTUBULE ASSOCIATED
1391	1cz7	A	1	231	1e-38	0.19	1.00		MICROTUBULE MOTOR	CONTRACTILE PROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									PROTEIN NCD; CHAIN: A, B, C, D;	NCD, CLARET SEGREGATIONAL PROTEIN; NCD CRYSTAL STRUCTURE, MICROTUBULE MOTORS, KINESIN 2 SUPERFAMILY, CONTRACTILE PROTEIN
1391	1ez7	A	1	238	6e-66	0.24	1.00		MICROTUBULE MOTOR PROTEIN NCD; CHAIN: A, B, C, D;	CONTRACTILE PROTEIN NCD, CLARET SEGREGATIONAL PROTEIN; NCD CRYSTAL STRUCTURE, MICROTUBULE MOTORS, KINESIN 2 SUPERFAMILY, CONTRACTILE PROTEIN
1391	2kin	A	1	146	1.7e-35	0.08	0.90		KINESIN; CHAIN: A, B;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
1391	2kin	A	6	146	1.8e-37	0.12	0.60		KINESIN; CHAIN: A, B;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
1391	2kin	B	160	261	6.8e-20	-0.24	0.47		KINESIN; CHAIN: A, B;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
1391	2kin	B	161	257	6e-31			51.11	KINESIN; CHAIN: A, B;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
1391	2kin	B	162	244	6e-31	-0.25	1.00		KINESIN; CHAIN: A, B;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
1391	2ncd	A	1	231	5.1e-39	0.11	1.00		KINESIN MOTOR NCD; CHAIN: A;	CONTRACTILE PROTEIN KINESIN, MICROTUBULE-BASED MOTOR, NCD, CONTRACTILE PROTEIN
1391	2ncd	A	1	236	1e-66	0.16	1.00		KINESIN MOTOR NCD; CHAIN: A;	CONTRACTILE PROTEIN KINESIN, MICROTUBULE-BASED MOTOR, NCD, CONTRACTILE PROTEIN



Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1391	3kar		1	236	4e-62			69.80	KINESIN-LIKE PROTEIN KAR3; CHAIN: NULL;	CONTRACTILE PROTEIN CONTRACTILE PROTEIN, KAR3, KINESIN-RELATED PROTEIN, MOTOR 2 PROTEIN, ATPASE, P-LOOP, MICROTUBULE BINDING PROTEIN
1391	3kar		1	236	4e-62	0.20	1.00		KINESIN-LIKE PROTEIN KAR3; CHAIN: NULL;	CONTRACTILE PROTEIN CONTRACTILE PROTEIN, KAR3, KINESIN-RELATED PROTEIN, MOTOR 2 PROTEIN, ATPASE, P-LOOP, MICROTUBULE BINDING PROTEIN
1391	3kar		9	233	3.4e-40	0.12	1.00		KINESIN-LIKE PROTEIN KAR3; CHAIN: NULL;	CONTRACTILE PROTEIN CONTRACTILE PROTEIN, KAR3, KINESIN-RELATED PROTEIN, MOTOR 2 PROTEIN, ATPASE, P-LOOP, MICROTUBULE BINDING PROTEIN
1391	3kin	B	164	244	1.2e-29	-0.01	0.99		KINESIN HEAVY CHAIN; CHAIN: A, B, C, D;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
1391	3kin	B	164	277	5.1e-21	-0.46	0.82		KINESIN HEAVY CHAIN; CHAIN: A, B, C, D;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
1391	3kin	B	164	282	1.2e-29			57.01	KINESIN HEAVY CHAIN; CHAIN: A, B, C, D;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
1398	1erj	A	117	362	1.7e-53	0.20	0.17		TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	TRANSCRIPTION INHIBITOR BETA-PROPELLER
1398	1erj	A	132	469	1.7e-64	0.37	0.60		TRANSCRIPTIONAL REPRESSOR	TRANSCRIPTION INHIBITOR

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1398	1ejj	A	195	512	1e-65	0.72	1.00		TUPI; CHAIN: A, B, C; TRANSCRIPTIONAL REPRESSOR	BETA-PROPELLER TRANSCRIPTION INHIBITOR
1398	1ejj	A	285	599	1.7e-62	0.30	0.09		TUPI; CHAIN: A, B, C; TRANSCRIPTIONAL REPRESSOR	BETA-PROPELLER TRANSCRIPTION INHIBITOR
1398	1got	B	117	418	3.4e-57	0.47	0.66		GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
1398	1got	B	145	509	5.1e-74			118.79	GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
1398	1got	B	185	509	5.1e-74	0.68	0.99		GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1398	1got	B	269	599	8.5e-53	0.08	-0.05		GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	SIGNAL TRANSDUCTION COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
1401	1aci		60	134	1e-26	-0.22	0.83		L11 RIBOSOMAL PROTEIN; CHAIN: NULL;	RIBOSOMAL PROTEIN L11-C76, RIBOSOMAL PROTEIN
1401	1mms	A	18	133	1.7e-47	0.25	1.00		RIBOSOMAL PROTEIN L11; CHAIN: A, B; 23S RIBOSOMAL RNA; CHAIN: C, D;	RIBOSOME RNA-PROTEIN COMPLEX, RNA, RIBOSOME, TRANSLOCATION, 2 THIOSTREPTON
1401	1mms	B	63	133	1.7e-27	0.50	1.00		RIBOSOMAL PROTEIN L11; CHAIN: A, B; 23S RIBOSOMAL RNA; CHAIN: C, D;	RIBOSOME RNA-PROTEIN COMPLEX, RNA, RIBOSOME, TRANSLOCATION, 2 THIOSTREPTON
1401	1qa6	A	63	131	3.4e-24	0.20	0.89		RIBOSOMAL PROTEIN L11; CHAIN: A, B; 58 NUCLEOTIDE RIBOSOMAL RNA DOMAIN; CHAIN: C, D;	RIBOSOME RIBOSOMAL RNA, TERTIARY STRUCTURE RNA-PROTEIN INTERACTION, 2 MINOR GROOVE BINDING, ANTIBIOTIC BINDING, RIBOSOME
1404	1alh	A	404	484	4.8e-40	0.26	1.00		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX	COMPLEX (ZINC FINGER/DNA) COMPLEX

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	(ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1404	1alh	A	404	484	5.1e-26	0.27	1.00		QGR ZINC FINGER PEPTIDE; CHAIN: A; DUPLICATION OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1404	1alh	A	432	540	4.8e-33	0.12	0.51		QGR ZINC FINGER PEPTIDE; CHAIN: A; DUPLICATION OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1404	1alh	A	544	625	2.4e-44	0.21	1.00		QGR ZINC FINGER PEPTIDE; CHAIN: A; DUPLICATION OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1404	1alh	A	656	736	1.2e-42	0.64	1.00		QGR ZINC FINGER PEPTIDE; CHAIN: A; DUPLICATION OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1404	1alh	A	656	736	6.8e-31	0.61	1.00		QGR ZINC FINGER PEPTIDE; CHAIN: A; DUPLICATION OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1404	1mey	C	123	204	5.1e-40	0.23	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1404	1mey	C	151	232	1.4e-41	0.56	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1404	1mey	C	179	260	6.8e-43	0.26	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1404	1mey	C	207	288	1.7e-44	0.32	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1404	1mey	C	235	316	1.4e-45	0.53	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1404	1mey	C	263	344	1.1e-45	0.53	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	(ZINC FINGER/DNA)  COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1404	1mey	C	319	400	1.2e-44	0.41	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1404	1mey	C	319	400	8.4e-46	0.41	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1404	1mey	C	347	428	1.2e-44	0.64	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1404	1mey	C	347	428	1.7e-44	0.64	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER	COMPLEX (ZINC FINGER/DNA) ZINC FINGER,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									PROTEIN; CHAIN: C, F, G;	PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1404	1mey	C	375	456	2.4e-43	0.29	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1404	1mey	C	375	456	5.1e-43	0.29	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1404	1mey	C	403	484	3.4e-43	0.50	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1404	1mey	C	431	512	1.7e-42	0.49	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1404	1mey	C	431	540	2.4e-36	-0.10	0.99		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	STRUCTURE, COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1404	1mey	C	459	540	5.1e-44	0.30	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1404	1mey	C	459	568	7.2e-37	-0.18	0.93		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1404	1mey	C	487	568	8.5e-46	0.51	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1404	1mey	C	515	596	5.1e-47	0.26	1.00		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA)



Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1404	1mey	C	543	624	8.5e-48	0.82	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1404	1mey	C	571	652	3.4e-49	0.59	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1404	1mey	C	655	736	6.8e-51	0.58	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1404	1mey	C	67	148	1.7e-37	-0.13	0.04		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1404	1mey	C	683	764	3.4e-51	0.66	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1404	1mey	C	711	792	6.8e-51	0.48	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1404	1mey	C	711	793	3.4e-51			109.39	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1404	1mey	C	739	820	6.8e-51	0.47	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1404	1mey	C	767	848	3.4e-50	0.56	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1404	1mey	C	795	876	1e-49	0.57	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1404	1mey	C	823	880	1.7e-33	0.45	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1404	1mey	C	95	176	1.4e-39	-0.14	0.95		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1404	1mey	G	849	876	1.7e-12	1.17	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1404	1mey	G	849	876	4.8e-13	1.17	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1404	1tf6	A	124	288	1.1e-62	-0.10	0.83		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1404	1tf6	A	152	316	1.1e-68	0.09	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1404	1tf6	A	180	344	2.4e-72	0.11	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1404	1ff6	A	208	372	4.8e-72	-0.05	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1404	1ff6	A	235	403	4.8e-74			126.07	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1404	1ff6	A	236	382	8.5e-35	0.16	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1404	1ff6	A	236	400	4.8e-74	0.13	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1404	1ff6	A	320	469	1.7e-34	0.33	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1404	1ff6	A	376	568	2.4e-63	-0.11	0.90		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1404	1ff6	A	432	578	5.1e-34	0.08	0.86		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1404	1ff6	A	488	633	6.8e-36	0.12	0.96		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN:	COMPLEX (TRANSCRIPTION REGULATION/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1404	1ff6	A	544	689	1.7e-36	0.12	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1404	1ff6	A	544	708	4.8e-75	0.17	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1404	1ff6	A	572	736	4.8e-76	-0.11	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1404	1ff6	A	600	745	3.4e-39	0.20	1.00		TFIIIA; CHAIN: A, D; 5S	COMPLEX (TRANSCRIPTION

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	REGULATION/DNA COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1404	1ff6	A	628	792	7.2e-72	0.26	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1404	1ff6	A	712	858	1.7e-37	0.37	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1404	1ff6	A	712	876	1.2e-71	0.18	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN



Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1404	1tf6	A	768	878	1.7e-30	0.23	0.98		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1404	1tf6	A	96	246	8.5e-31	-0.14	0.74		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1404	1ubd	C	104	204	8.4e-35	0.18	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1404	1ubd	C	126	232	6.8e-28	0.32	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1404	1ubd	C	128	232	2.4e-44	0.00	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1404	1ubd	C	156	260	1.1e-47	0.11	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1404	1ubd	C	205	316	6e-54	0.27	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1404	1ubd	C	261	372	3.6e-54	0.39	1.00		YY1; CHAIN: C; ADENO-	COMPLEX (TRANSCRIPTION REGULATION/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1404	1ubd	C	291	401	3.6e-54			98.61	YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1404	1ubd	C	299	400	3.4e-31	0.39	1.00		YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1404	1ubd	C	345	456	2.4e-52	-0.03	1.00		YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1404	1ubd	C	383	484	1.5e-29	0.22	0.99		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1404	1ubd	C	401	541	2.4e-44	-0.05	0.53		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1404	1ubd	C	406	512	1.7e-29	0.03	0.81		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1404	1ubd	C	457	596	2.4e-49	0.12	0.99		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1404	1ubd	C	467	568	6.8e-30	0.17	0.98		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1404	1ubd	C	490	596	1.5e-31	0.53	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1404	1ubd	C	523	624	1.7e-33	-0.01	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1404	1ubd	C	542	652	1.1e-55	0.27	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1404	1ubd	C	551	652	6.8e-34	0.18	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1404	1ubd	C	597	708	8.4e-56	0.24	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1404	1ubd	C	625	737	4.8e-56	0.36	1.00		YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1404	1ubd	C	653	764	2.4e-52	-0.03	1.00		YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1404	1ubd	C	663	764	6.8e-35	0.34	1.00		YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1404	1ubd	C	691	792	8.5e-35	0.03	1.00		YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									CHAIN: A, B;	INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1404	1ubd	C	70	176	3.4e-27	-0.35	0.72		YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1404	1ubd	C	709	820	1.1e-53	0.41	1.00		YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1404	1ubd	C	747	848	8.5e-35	0.36	1.00		YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3



Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										COMPLEX (TRANSCRIPTION REGULATION/DNA)
1404	1ubd	C	765	876	1.1e-53	0.36	1.00		YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1404	1ubd	C	775	876	3.4e-33	0.26	1.00		YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1404	2gli	A	123	262	2.4e-57	0.16	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1404	2gli	A	207	346	1.2e-69	0.27	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1404	2gli	A	263	402	1.2e-69			108.67	ZINC FINGER PROTEIN GLI1;	COMPLEX (DNA-BINDING

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									CHAIN: A; DNA; CHAIN: C, D;	PROTEIN/DNA FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1404	2gli	A	291	430	7.2e-69	0.54	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1404	2gli	A	319	458	4.8e-69	0.40	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1404	2gli	A	375	542	2.4e-61	-0.13	0.64		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1404	2gli	A	378	514	6.8e-29	0.19	0.94		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1404	2gli	A	431	626	6e-66	-0.29	0.11		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1404	2gli	A	459	595	8.5e-32	0.25	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1404	2gli	A	543	679	1e-34	0.22	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1404	2gli	A	571	710	1.2e-72	0.42	0.99		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1404	2gli	A	627	766	4.8e-70	0.26	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1404	2gli	A	635	763	1.2e-33	0.50	0.96		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1404	2gli	A	711	878	7.2e-70	0.25	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1404	2gli	A	719	847	1.2e-33	0.20	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1404	2gli	A	747	875	1.5e-33	0.50	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1404	2gli	A	95	231	3.4e-28	0.30	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1411	1dkg	A	297	399	0.0036	-0.23	0.03		NUCLEOTIDE EXCHANGE FACTOR GRPE; CHAIN: A, B; MOLECULAR CHAPERONE DNAK; CHAIN: D;	COMPLEX (HSP24/HSP70) HSP70, GRPE, MOLECULAR CHAPERONE, NUCLEOTIDE EXCHANGE 2 FACTOR, COILED-COIL, COMPLEX (HSP24/HSP70)
1417	1aoa		966	1065	4.4e-27	0.47	0.53		T-FIMBRIN; CHAIN: NULL;	ACTIN-BINDING PROTEIN ACTIN-BINDING PROTEIN, CALCIUM-BINDING, PHOSPHORYLATION
1417	1bhd	A	966	1065	4.4e-33	0.40	1.00		UTROPHIN; CHAIN: A, B;	STRUCTURAL PROTEIN CALPONIN HOMOLGY, ACTIN BINDING, STRUCTURAL PROTEIN
1417	1bhd	A	968	1067	1.4e-13	0.48	1.00		UTROPHIN; CHAIN: A, B;	STRUCTURAL PROTEIN CALPONIN HOMOLGY, ACTIN BINDING,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1417	1bkr	A	965	1070	1.7e-21	0.56	1.00		SPECTRIN BETA CHAIN; CHAIN: A;	STRUCTURAL PROTEIN ACTIN-BINDING CALPONIN HOMOLOGY (CH) DOMAIN; FILAMENTOUS ACTIN-BINDING DOMAIN, CYTOSKELETON
1417	1d0s	A	127	444	2.2e-12	0.11	-0.19		NICOTINATE MONONUCLEOTIDE:5,6- CHAIN: A;	TRANSFERASE DINUCLEOTIDE-BINDING MOTIF, PHOSPHORIBOSYL TRANSFERASE
1417	1dxx	A	968	1066	3.4e-12	0.46	1.00		DYSTROPHIN; CHAIN: A, B, C, D;	STRUCTURAL PROTEIN DYSTROPHIN, MUSCULAR DYSTROPHY, CALPONIN HOMOLOGY DOMAIN, 2 ACTIN-BINDING, UTROPHIN
1417	1qag	A	966	1065	6.6e-31	0.29	1.00		UTROPHIN ACTIN BINDING REGION; CHAIN: A, B;	STRUCTURAL PROTEIN CALPONIN HOMOLOGY DOMAIN, DOMAIN SWAPPING, ACTIN BINDING, 2 UTROPHIN, DYSTROPHIN, STRUCTURAL PROTEIN
1417	1qag	A	968	1067	1.4e-13	0.58	1.00		UTROPHIN ACTIN BINDING REGION; CHAIN: A, B;	STRUCTURAL PROTEIN CALPONIN HOMOLOGY DOMAIN, DOMAIN SWAPPING, ACTIN BINDING, 2 UTROPHIN, DYSTROPHIN, STRUCTURAL PROTEIN
1418	1btk	A	6	119	1.7e-11	-0.07	0.59		BRUTON'S TYROSINE KINASE; CHAIN: A, B;	TRANSFERASE BRUTON'S AGAMMAGLOBULINEMIA TYROSINE KINASE, BTK;

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										TRANSFERASE, PH DOMAIN, BTK MOTIF, ZINC BINDING, X-LINKED 2
1418	1bm		8	115	8.5e-15	0.13	0.13		BETA-SPECTRIN; 1BTN 4 CHAIN: NULL; 1BTN 5	AGAMMAGLOBULINEMIA, TYROSINE-PROTEIN KINASE
1418	1dro		9	113	6.8e-11	-0.13	0.89		BETA-SPECTRIN; 1DRO 6 CHAIN: NULL; 1DRO 7	SIGNAL TRANSDUCTION PROTEIN
1418	1fao	A	7	113	3.4e-16	0.57	0.90		DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3-CHAIN: A;	CYTOSKELETON
										SIGNALING PROTEIN DAPP1, PHISH, BAM32; PLECKSTRIN, 3- PHOSPHOINOSITIDES, INOSITOL TETRAKISPHOSPHATE 2 SIGNAL TRANSDUCTION PROTEIN, ADAPTOR PROTEIN
1418	1fb8	A	7	113	3.4e-16	0.37	0.92		DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3-CHAIN: A;	SIGNALING PROTEIN DAPP1, PHISH, BAM32; PLECKSTRIN, 3- PHOSPHOINOSITIDES, INOSITOL TETRAKISPHOSPHATE 2 SIGNAL TRANSDUCTION PROTEIN, ADAPTOR PROTEIN
1418	1fgy	A	6	123	8.5e-17	-0.03	0.39		GRP1; CHAIN: A;	SIGNALING PROTEIN ARF1 GUANINE NUCLEOTIDE EXCHANGE FACTOR AND

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1418	1pls		5	123	1.1e-18	0.34	0.35		PHOSPHORYLATION PLECKSTRIN (N-TERMINAL PLECKSTRIN HOMOLOG DOMAIN) MUTANT 1PLS 3 WITH LEU GLU (HIS)6 ADDED TO THE C TERMINUS 1PLS 4 (INS(G105-LEHHHHH)) (NMR, 25 STRUCTURES) 1PLS 5	PH DOMAIN
1418	1pls		7	118	5.1e-14	0.48	0.66		PHOSPHORYLATION PLECKSTRIN (N-TERMINAL PLECKSTRIN HOMOLOG DOMAIN) MUTANT 1PLS 3 WITH LEU GLU (HIS)6 ADDED TO THE C TERMINUS 1PLS 4 (INS(G105-LEHHHHH)) (NMR, 25 STRUCTURES) 1PLS 5	
1418	1qgg	A	5	114	5.1e-16	0.40	0.98		INSULIN RECEPTOR SUBSTRATE 1; CHAIN: A, B;	SIGNAL TRANSDUCTION IRS-1; BETA-SANDWHICH, SIGNAL TRANSDUCTION
1418	1qgg	A	5	151	6.6e-23	0.06	0.30		INSULIN RECEPTOR SUBSTRATE 1; CHAIN: A, B;	SIGNAL TRANSDUCTION IRS-1; BETA-SANDWHICH, SIGNAL TRANSDUCTION
1419	1btk	A	6	119	6.8e-10	0.02	0.27		BRUTON'S TYROSINE KINASE; CHAIN: A, B;	TRANSFERASE BRUTON'S AGAMMAGLOBULINEMIA TYROSINE KINASE, BTK; TRANSFERASE, PH DOMAIN, BTK MOTIF, ZINC BINDING, X-LINKED 2 AGAMMAGLOBULINEMIA,